

FIGURE 1

Human DNase I

LOCUS HUMDNASEI 1039 bp mRNA PRI 06-MAR-1995
 DEFINITION Human DNase I mRNA, complete cds.
 ACCESSION M55983
 VERSION M55983.1 GI:181623
 KEYWORDS DNase I.
 SOURCE Human pancreas, cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1039)
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672

FEATURES Location/Qualifiers
 source 1..1039
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 /db_xref="taxon:9606"
 /clone="hDNase-18-1"
 /tissue_type="pancreas"
 sig_peptide 160..225
 /gene="DNase I"
 CDS 160..1008
 /gene="DNase I"
 /codon_start=1
 /product="DNase I"
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 /db_xref="GI:181624"
 /translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
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 LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
 DAVAEIDALYDVYLDVQEKWGLEDMMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLI
 PDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAI SDHYP
 VEVMLK"
 gene 160..1008
 /gene="DNase I"
 mat_peptide 226..1005
 /gene="DNase I"
 /product="DNase I"

BASE COUNT 226 a 305 c 282 g 226 t

ORIGIN

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121 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg
181 ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgacgcc
241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
301 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg
361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
541 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc
601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgatcatgtg
721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
781 ctgtggacaa gcccacacct ccagtggctg atccccgaca gcgctgacac cacagctaca
841 cccacgcact gtgcctatga caggatcggt gttgcaggga tgctgctccg aggcgcggtt
901 gttcccgact cggctcttcc ctttaacttc caggctgctt atggcctgag tgaccaactg
961 gcccaagcca tcagtgaaca ctatccagtg gaggtgatgc tgaagtgage agcccctccc
1021 cacaccagtt gaactgcag
```

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FIGURE 2

Human DNase I cDNA

(A)

LOCUS MHDNASE.DN 783 bp mRNA PRI 06-MAR-1995
 DEFINITION Human DNase I mRNA, complete cds, Mature sequence modified to remove NarI site
 ACCESSION M55963
 NID q181623
 KEYWORDS DNase I.
 SOURCE Human pancreas, cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1039)
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 FEATURES
 source Location/Qualifiers
 1..1039
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="hDNase-18-1"
 /tissue_type="pancreas"
 sig_peptide 160..225
 /gene="DNase I"
 CDS 160..1008
 /gene="DNase I"
 /codon_start=1
 /product="DNase I"
 /db_xref="PID:q181624"
 /translation="LKIAAFNIQTGETKMSNATLVSYIVQILSRVDIALVQEVDRSH
 LTAVGKLLDNLNQDAPDTYHYVSEPLGRNSYKERYLFVYRDPQVSAVDSYYDDGCE
 PCGNDFNREPAIVRFFSRFTEVREFAIIVPLHAAPGDVAEIDALYDVYLDVQEKWGL
 EDVIMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG
 MLLRGAVVPDSALFFNFQAAYGLSDQLAQAI SDHYPVEVMT.K"
 gene 160..1008
 /gene="DNase I"
 mat_peptide 226..1005
 /gene="DNase I"
 /product="DNase I"
 BASE COUNT 168 a 236 c 220 g 159 t
 ORIGIN

1 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
 61 CTCGTCAGCI ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
 121 AGAGACAGCC ACCTGACTGC CCGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
 181 GACACCTATC ACTACGTGOT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
 241 CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
 301 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
 361 CCGTTCACAG AGGTCAGGGA GTTGGCCATT GTTCCCTGTC ATGCGGCCCC GGGGGACGCA
 421 GTAGCCGAGA TCGACGCTCI CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 481 GAGGACGTCA IGTGTATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCAG
 541 TGGTCAICCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
 601 GACACCCACG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
 661 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCTTTTA ACTTCCAGGC TGCCTATGGC
 721 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
 781 TGA

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FIGURE 2(B)

LOCUS PAS155_GB. 858 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

Location/Qualifiers

frag 10..75

/note="160 to 225 of Untitled1"

frag <10..>75

/note="1 to 1039 of M55983.DNA [Split]"

source <10..>75

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="hDNase-18-1"

/tissue_type="pancreas [Split]"

sig_peptide 10..75

/gene="DNase I"

CDS 10..>75

/gene="DNase I"

/codon_start="1"

/product="DNase I"

/db_xref="PID:g181624"

/translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
SYIVQILSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERY
LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
D... [Split]"

gene 10..>75

/gene="DNase I [Split]"

frag 76..858

/note="1 to 783 of mod humanDNaseI"

frag 76..858

/note="1 to 72 of 104linker"

frag join(76..>129,<131..147)

/note="1 to 72 of 103linker [Split]"

frag join(76..>126,<127..>129,<131..147)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 177 A 260 C 251 G 170 T 0 OTHER

ORIGIN

1 GCCGCCACCA TGAGGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC GGCCCTACTG

61 CAGGGGGGCG TGTCCTTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG

121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC

181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC

241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC

301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC

361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT

421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG

481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA

541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT

601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCGCCACCTT CCAGTGGCTG

661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG

721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC

781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG

841 GAGGTGATGC TGAAGTGA

FIGURE 3

(A) pAS6 - light chain

LOCUS HMFG1LC2.D 721 bp DNA
 DEFINITION HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.
 ACCESSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (BASES 1 TO 342)
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 ETC
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT SCANNED IN FROM JOURNAL
 FEATURES
 SITES

This is the sequence of the HMFG1 light chain gene with the Vnp leader sequence attached. Translate from residue 1. Note residue 399 is T > A in all clones leading to R133 silent mutation (T in Verhoeyen paper)

BASE COUNT 197 a 202 c 182 g 140 t
 ORIGIN 7

LEADER SEQ

| | | | | | | |
|-----|------------|------------|------------|------------|------------|------------|
| 1 | ATGGGATGGA | GCTGTATCAT | CCTCTTCTTG | GTAGCAACAG | CTACAGGTGT | CCACTCCGAC |
| 61 | ATCCAGATGA | CCCAGAGCCC | AAGCAGCCTG | AGCGCCAGCG | TGGGTGACAG | AGTGACCATC |
| 121 | ACCTGTAAGT | CCAGTCAGAG | CCTTTTATAT | AGTAGCAATC | AAAAGATCTA | CITGGCCTGG |
| 181 | TACCAGCAGA | AGCCAGGTAA | GGCTCCAAAG | CTGCTGATCT | ACTGGGCATC | CACTAGGGAA |
| 241 | TCTGGTGTGC | CAAGCAGATT | CAGCGGTAGC | GGTAGCGGTA | CCGACTTCAC | CTTCACCATC |
| 301 | AGCAGCCTCC | AGCCAGAGGA | CATCGCCACC | TACTACTGCC | AGCAATATTA | TAGATATCCT |
| 361 | CGGACGTTCC | GCCAAGGGAC | CAAGGTGGAA | ATCAAACGAA | CTGTGGCTGC | ACCATCTGTC |
| 421 | TTCATCTTCC | CGCCATCTGA | TGAGCAGTTG | AAATCTGGAA | CTGCCTCTGT | TGTGTGCCTG |
| 481 | CTGAATAACT | ICTATCCCAG | AGAGGCCAAA | GTACAGTGGA | AGGTGGATAA | CGCCCTCCAA |
| 541 | ICGGGTAACT | CCCAGGAGAG | TGTCACAGAG | CAGGACAGCA | AGGACAGCAC | CTACAGCCTC |
| 601 | AGCAGCACCC | TGACGCTGAG | CAAAGCAGAC | TACGAGAAAC | ACAAAGTCTA | CGCCTGCGAA |
| 661 | GTCACCCATC | AGGGCCTGAG | CTCGCCCGTC | ACAAAGAGCT | TCAACAGGGG | AGAGTGTTAG |
| 721 | A | | | | | |

//

Figure 3(B)

LOCUS HHMFG1KLC_ 730 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
 frag 10..730
 /note="1 to 721 of hHMFG1light chain"
 frag 10..730
 /note="1 to 72 of 104linker"
 frag join(10..>63,<65..81)
 /note="1 to 72 of 103linker [Split]"
 frag join(10..>60,<61..>63,<65..81)
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 198 A 208 C 184 G 140 T 0 OTHER
 ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
 121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
 181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
 241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC
 301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
 361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 661 GCCTGCGAAG TCACCCATCA GGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 721 GAGTGTTAGA

//

500
 1000

Figure 3 (c)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCILELVATATGVHSDIQMTQSPSSLSASVGDRVITITCKSSQSL
LYSSNQKIYLA WYQQKPGKAPKLLIWASTRESGVPSRFSGSGSGT
DFTFTISLQPEDATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI
FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSSTLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFN
RGE C

FIGURE 3

(0) pAS6 - heavy chain

LOCUS HHMFGLHC.D 1404 bp DNA
 DEFINITION HUMANISED HHMFGL heavy chain
 ACCESSION HHMFGLH
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HHMFGL etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT VH domain SCANNED IN FROM JOURNAL
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 333 a 439 c 379 g 253 t
 ORIGIN ?

← LINKER →

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TCCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGCCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCTTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAGTCA
541 GGCGCCCTGA CCAGCGCGGT GCACACCTTC CCGGTGTGTC TACAGTCTTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCGAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAA TCCTGGGGGG ACCGTCAGTC
781 TTCTCTTCC CCCCANAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTGACA
841 TCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCAGTAC
961 CGTGTGGTCA GCGTCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCRAGAGAGC
1381 CTCTCCCTGT CTCCGGGTAA ATGA
  
```

Antibody Dnae fusions made here (eg pAS 34-39.)

End of lower hinge region of heavy chain. PAPE Amino Acid SEQ. Fab₂ fusions were made at this point.

Those with HYBRID HINGES ARE ALTERED FURTHER UP

ie.

THIS PART GACAAACTGACACA
 is → D K T H T

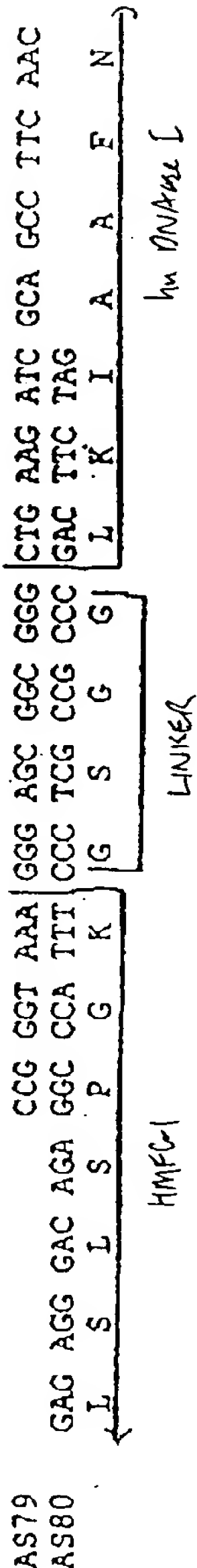
AFTER THIS SEQUENCE YOU GET THE

HYBRID HINGE & LINKER SEQUENCES

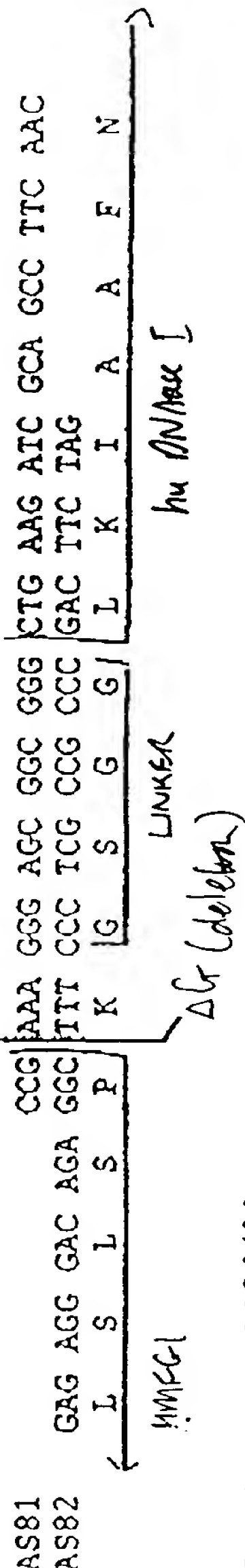
Then Dnae I (eg Fab-Dnae construct pAS302)

(A.) Oligos involved in the fusion of whole antibody-DNase

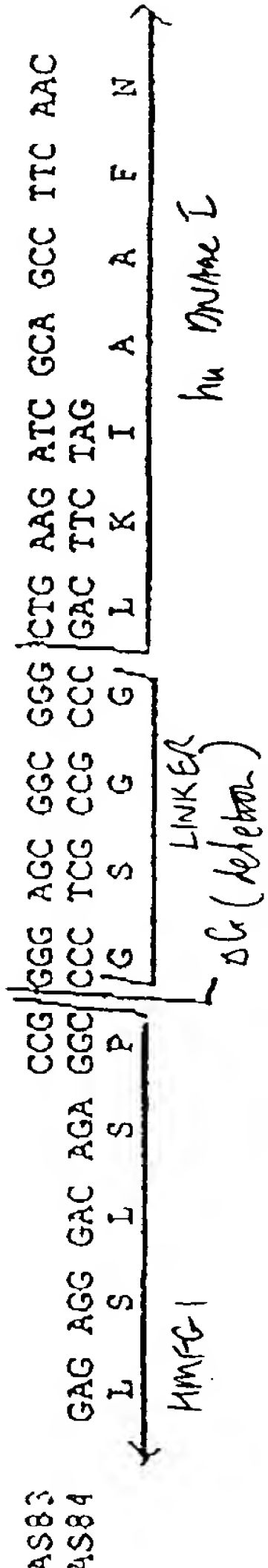
Constructs PAS34/37



Constructs PAS35/38

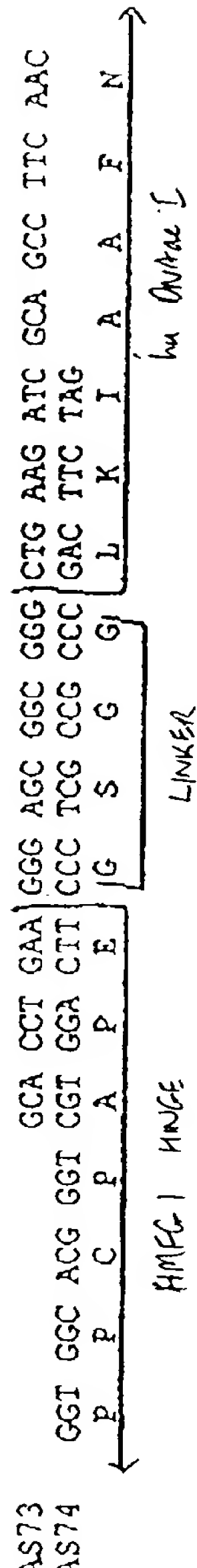


Constructs PAS36/39



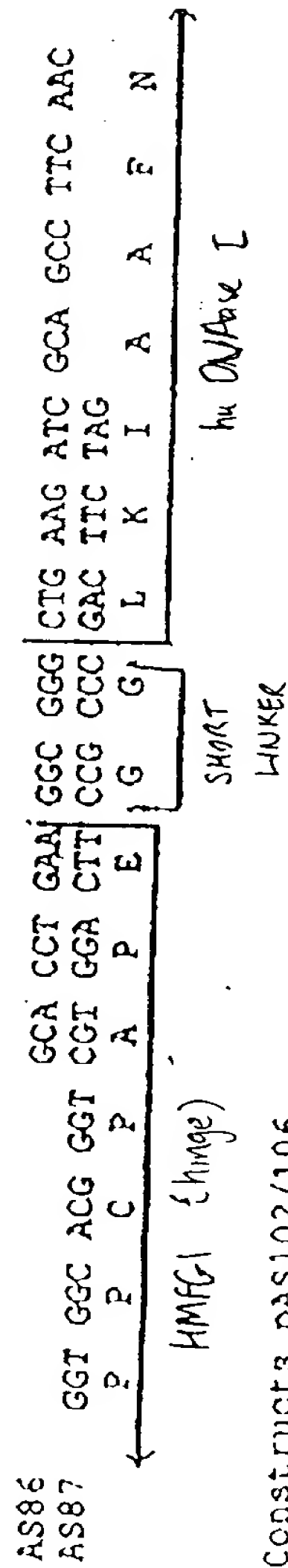
Oligos involved in the fusion of Fab'2-DNase I

Constructs PAS23/27

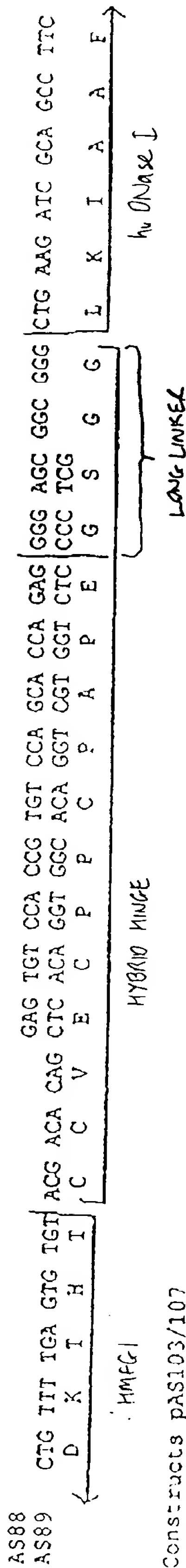


(B.) Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

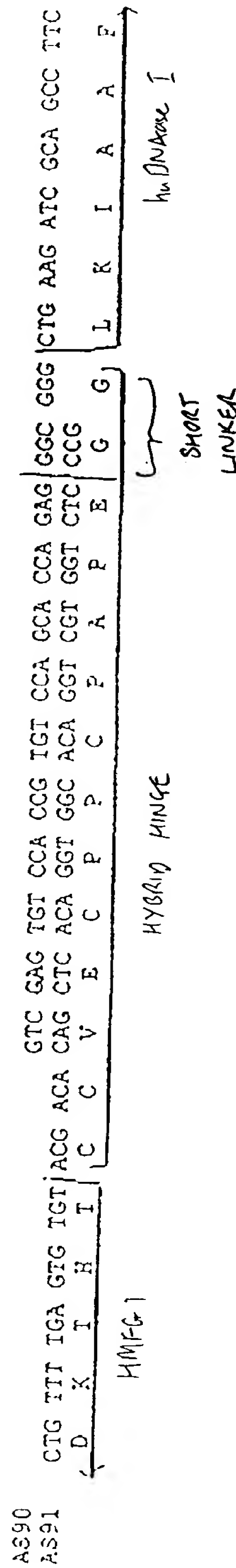
Constructs PAS101/105



Constructs PAS102/106



Constructs PAS103/107



(A) pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 344 a 468 c 434 g 308 t
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGAATACTTC CCCGAACCGG TGACGGGTGC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAG GGAGCGGCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
1021 TACAGGCCTG ACCAGGTGTC TCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCCTCTC CCGGTTTACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTT CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

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Figure 5(B)

LOCUS FDDNASE23_ 1554 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<787..1554)
 /note="1 to 1554 of 23.dna [Split]"
 frag 721..786
 /note="1 to 66 of 23/27linker"
 frag join(721..>735,<736..786)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 344 A 466 C 435 G 309 T 0 OTHER
 ORIGIN -

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1  ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
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781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
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1021 TACAGGCCTG ACCAGGTGTC TGCAGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCCTTCTC CCGGTTTACA
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 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers

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 frag 730..795
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 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 345 A 472 C 437 G 309 T 0 OTHER
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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
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File : PAS23.DNA
Range : 1 - 1554 Mode : Normal
Codon Table : UniProt

FIGURE S(D)

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| | 9 | | 18 | | 27 | | 36 | | 45 | | 54 | | | | | | | |
| 5' | ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TTC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | GTC | CAC |
| | M | G | W | S | C | I | I | L | F | L | V | A | T | A | T | G | V | H |
| | | 63 | | 72 | | 81 | | 90 | | 99 | | 108 | | | | | | |
| | TCC | CAG | GTG | CAG | CTG | GTG | CAG | TCT | GGG | GCA | GAG | GTG | AAA | AAG | CCT | GGG | GCC | TCA |
| | S | Q | V | Q | L | V | Q | S | G | A | E | V | K | K | P | G | A | S |
| | | 117 | | 126 | | 135 | | 144 | | 153 | | 162 | | | | | | |
| | GTG | AAG | GTG | TCC | TGC | AAG | GCT | TCT | GGC | TAC | ACC | TTC | AGT | GCC | TAC | TGG | ATA | GAG |
| | V | K | V | S | C | K | A | S | G | Y | T | F | S | A | Y | W | I | E |
| | | 171 | | 180 | | 189 | | 198 | | 207 | | 216 | | | | | | |
| | TGG | GTG | CGC | CAG | GCT | CCA | GGA | AAG | GGC | CTC | GAG | TGG | GTC | GGA | GAG | ATT | TTA | CCT |
| | W | V | R | Q | A | P | G | K | G | L | E | W | V | G | E | I | L | P |
| | | 225 | | 234 | | 243 | | 252 | | 261 | | 270 | | | | | | |
| | GGA | AGT | AAT | AAT | TCT | AGA | TAC | AAT | GAG | AAG | TTC | AAG | GGC | CGA | GTG | ACA | GTC | ACT |
| | G | S | N | N | S | R | Y | N | E | K | F | K | G | R | V | T | V | T |
| | | 279 | | 288 | | 297 | | 306 | | 315 | | 324 | | | | | | |
| | AGA | GAC | ACA | TCC | ACA | AAC | ACA | GCC | TAC | ATG | GAG | CTC | AGC | AGC | CTG | AGG | TCT | GAG |
| | R | D | T | S | T | N | T | A | Y | M | E | L | S | S | L | R | S | E |
| | | 333 | | 342 | | 351 | | 360 | | 369 | | 378 | | | | | | |
| | GAC | ACA | GCC | GTC | TAT | TAC | TGT | GCA | AGA | TCC | TAC | GAC | TTT | GCC | TGG | TTT | GCT | TAC |
| | D | T | A | V | Y | Y | C | A | R | S | Y | D | F | A | W | F | A | Y |
| | | 387 | | 396 | | 405 | | 414 | | 423 | | 432 | | | | | | |
| | TGG | GGC | CAA | GGG | ACT | CTG | GTC | ACA | GTC | TCC | TCA | GCC | TCC | ACC | AAG | GGC | CCA | TCG |
| | W | G | Q | G | T | L | V | T | V | S | S | A | S | T | K | G | P | S |
| | | 441 | | 450 | | 459 | | 468 | | 477 | | 486 | | | | | | |
| | GTC | TTC | CCC | CTG | GCA | CCC | TCC | TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG |
| | V | F | P | L | A | P | S | S | K | S | T | S | G | G | T | A | A | L |
| | | 495 | | 504 | | 513 | | 522 | | 531 | | 540 | | | | | | |
| | GGC | TGC | CTG | GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA |
| | G | C | L | V | K | D | Y | F | P | E | P | V | T | V | S | W | N | S |
| | | 549 | | 558 | | 567 | | 576 | | 585 | | 594 | | | | | | |
| | GGC | GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA |
| | G | A | L | T | S | G | V | H | T | F | P | A | V | L | Q | S | S | G |

- 1 -

| | | | | | |
|-------------------------------------|-------------------------|---------------------|-----------------|------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC AGC | AGC GTG GTG ACC GTG CCC | TCC AGC AGC TTG GGC | ACC CAG | | |
| L Y S L S S V V T V P S S S L G T Q | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC AAC | GTG AAT CAC AAG CCC | AGC AAC ACC AAG GTG | GAC AAG AAA | | |
| T Y I C N V N H K P S N T K V D K K | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT | TGT GAC AAA ACT CAC | ACA TGC CCA CCG TGC | CCA GCA CCT | | |
| V E P K S C D K T H T C P P C P A P | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| GAA GGG AGC GGC GGG | CTG AAG ATC GCA GCC | TTC AAC ATC CAG ACA | TTT GGG GAG | | |
| E G S G G L K I A A F N I Q T F G E | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| ACC AAG ATG TCC AAT | GCC ACC CTC GTC AGC | TAC ATT GTG CAG ATC | CTG AGC CGC | | |
| T K M S N A T L V S Y I V Q I L S R | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| TAC GAC ATC GCC CTG | GTC CAG GAG GTC AGA | GAC AGC CAC CTG ACT | GCC GTG GGG | | |
| Y D I A L V Q E V R D S H L T A V G | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| AAG CTG CTG GAC AAC | CTC AAT CAG GAC GCA | CCA GAC ACC TAT CAC | TAC GTG GTC | | |
| K L L D N L N Q D A P D T Y H Y V V | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| AGT GAG CCA CTG GGA | CGG AAC AGC TAT AAG | GAG CGC TAC CTG TTC | GTG TAC AGG | | |
| S E P L G R N S Y K E R Y L F V Y R | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| CCT GAC CAG GTG TCT | GCG GTG GAC AGC TAC | TAC TAC TAC GAT GAT | GGC TGC GAG CCC | | |
| P D Q V S A V D S Y Y Y D D G C E P | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| TGC GGG AAC GAC ACC | TTC AAC CGA GAG CCA | GCC ATT GTC AGG TTC | TTC TCC CGG | | |
| C G N D T F N R E P A I V R F F S R | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| TTC ACA GAG GTC AGG | GAG TTT GCC ATT GTT | CCC CTG CAT GCG GCC | CCG GGG GAC | | |
| F T E V R E F A I V P L H A A P G D | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|---|-----|-----|-----|-----|-----|-----|-----|-----|---|-----|-----|-----|-----|
| GCA | GTA | GCC | GAC | | GAC | GCT | CTC | TAT | GAC | GTC | TAC | CTG | | GTC | CAA | GAG | AAA |
| A | V | A | E | I | D | A | L | Y | D | V | Y | L | D | V | Q | E | K |

| | | | | | |
|------|------|------|------|------|------|
| 1251 | 1260 | 1269 | 1278 | 1287 | 1296 |
| TGG | GGC | TTG | GAG | GAC | GTC |
| ATG | TTG | ATG | GGC | GAC | TTC |
| AAT | GCG | GGC | TGC | AGC | TAT |
| W | G | L | E | D | V |
| M | L | M | G | D | F |
| N | A | G | C | S | Y |

| | | | | | |
|------|------|------|------|------|------|
| 1305 | 1314 | 1323 | 1332 | 1341 | 1350 |
| GTG | AGA | CCC | TCC | CAG | TGG |
| TCA | TCC | ATC | CGC | CTG | TGG |
| ACA | AGC | CCC | ACC | TTC | CAG |
| V | R | P | S | Q | W |
| S | S | I | R | L | W |
| T | S | P | T | F | Q |

| | | | | | |
|------|------|------|------|------|------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| TGG | CTG | ATC | CCC | GAC | AGC |
| GCT | GAC | ACC | ACA | GCT | ACA |
| CCC | ACG | CAC | TGT | GCC | TAT |
| W | L | I | P | D | S |
| A | D | T | T | A | T |
| P | T | H | C | A | Y |

| | | | | | |
|------|------|------|------|------|------|
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| GAC | AGG | ATC | GTG | GTT | GCA |
| GGG | ATG | CTG | CTC | CGA | GGG |
| GCC | GTT | GTT | CCC | GAC | TCG |
| D | R | I | V | V | A |
| G | M | L | L | R | G |
| A | V | V | P | D | S |

| | | | | | |
|------|------|------|------|------|------|
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| GCT | CTT | CCC | TTT | AAC | TTC |
| CAG | GCT | GCC | TAT | GGC | CTG |
| AGT | GAC | CAA | CTG | GCC | CAA |
| A | L | P | F | N | F |
| Q | A | A | Y | G | L |
| S | D | Q | L | A | Q |

| | | | |
|------|------|------|------|
| 1521 | 1530 | 1539 | 1548 |
| GCC | ATC | AGT | GAC |
| CAC | TAT | CCA | GTG |
| GAG | GTG | ATG | CTG |
| AAG | TGA | 3' | |
| A | I | S | D |
| H | Y | P | V |
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| K | * | | |

(A) pAS27

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 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 354 a 474 c 446 g 310 t
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LOCUS FDDNASE27_ 1584 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
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 /note="1 to 1584 of 27.dna [Split]"
 frag 721..786
 /note="1 to 66 of 23/27linker"
 frag join(721..>735,<736..786)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 354 A 472 C 447 G 311 T 0 OTHER
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LOCUS FDDNASE27K 1593 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

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/note="1 to 1584 of 27.dna [Split]"

frag 730..795

/note="1 to 66 of 23/27linker"

frag join(730..>744,<745..795)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 355 A 478 C 449 G 311 T 0 OTHER

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1021 CTGTTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC

1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC

1141 CGGTTACACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA

1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG

1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG

1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT

1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG

1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC

1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG

1561 GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT TGA

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File : PAS27.DNA
Range : 1 - 584 Mode : Normal
Codon Table : Universal

PURE 6(D)

| | | | | | |
|---|-----|-----|-----|-----|-----|
| 9 | 18 | 27 | 36 | 45 | 54 |
| ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC | | | | | |
| M G W S C I I L F L V A T A T G V H | | | | | |
| 63 | 72 | 81 | 90 | 99 | 108 |
| TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA | | | | | |
| S Q V Q L V Q S G A E V K K P G A S | | | | | |
| 117 | 126 | 135 | 144 | 153 | 162 |
| GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG | | | | | |
| V K V S C K A S G Y T F S A Y W I E | | | | | |
| 171 | 180 | 189 | 198 | 207 | 216 |
| TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT | | | | | |
| W V R Q A P G K G L E W V G E I L P | | | | | |
| 225 | 234 | 243 | 252 | 261 | 270 |
| GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT | | | | | |
| G S N N S R Y N E K F K G R V T V T | | | | | |
| 279 | 288 | 297 | 306 | 315 | 324 |
| AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG | | | | | |
| R D T S T N T A Y M E L S S L R S E | | | | | |
| 333 | 342 | 351 | 360 | 369 | 378 |
| GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC | | | | | |
| D T A V Y Y C A R S Y D F A W F A Y | | | | | |
| 387 | 396 | 405 | 414 | 423 | 432 |
| TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG | | | | | |
| W G Q G T L V T V S S A S T K G P S | | | | | |
| 441 | 450 | 459 | 468 | 477 | 486 |
| GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG | | | | | |
| V F P L A P S S K S T S G G T A A L | | | | | |
| 495 | 504 | 513 | 522 | 531 | 540 |
| GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA | | | | | |
| G C L V K D Y F P E P V T V S W N S | | | | | |
| 549 | 558 | 567 | 576 | 585 | 594 |
| GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA | | | | | |
| G A L T S G V H T F P A V L Q S S G | | | | | |

| | | | | | |
|---|---------------------------------|-----------------|------|------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC | AGC GTG GTG ACC GTG CCC TCC AGC | TTG GGC ACC CAG | | | |
| L Y S L S S V V T V P S S S L G T Q | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA | | | | | |
| T Y I C N V N H K P S N T K V D K K | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT | | | | | |
| V E P K S C D K T H T C P P C P A P | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG | | | | | |
| E G S G G L K I A A F N I Q T F G E | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC | | | | | |
| T K M S N A T L V S Y I V Q I L S R | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG | | | | | |
| Y D I A L V Q E V R D S H L T A V G | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC | | | | | |
| K L L D N L N Q D A P D T Y H Y V V | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG | | | | | |
| S E P L G R N S Y K E R Y L F V Y R | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC | | | | | |
| P D Q V S A V D S Y Y Y D D G C E P | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG | | | | | |
| C G N D T F N R E P A I V R F F S R | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC | | | | | |
| F T E V R E F A I V P L H A A P G D | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

| | | | | | | | | | | | | | | | | | |
|----------|----------|----------|----------|----------|-----|-----|------|-----|-----|------|-----|-----|----------|----------|----------|----------|----------|
| GCA | GTA | GCC | GAG | ATC | GAC | GCT | CTC | TAT | GAC | GTC | TAC | CTG | GAT | GTC | CAA | GAG | AAA |
| ----- | | | | | | | | | | | | | | | | | |
| A | V | A | E | | D | A | L | Y | D | V | Y | L | | V | Q | E | K |
| ----- | | | | | | | | | | | | | | | | | |
| 1251 | | | | 1260 | | | 1269 | | | 1278 | | | 1287 | | | 1296 | |
| TGG | GGC | TTG | GAG | GAC | GTC | ATG | TTG | ATG | GGC | GAC | TTC | AAT | GCG | GGC | TGC | AGC | TAT |
| ----- | | | | | | | | | | | | | | | | | |
| W | G | L | E | D | V | M | L | M | G | D | F | N | A | G | C | S | Y |
| ----- | | | | | | | | | | | | | | | | | |
| 1305 | | | | 1314 | | | 1323 | | | 1332 | | | 1341 | | | 1350 | |
| GTG | AGA | CCC | TCC | CAG | TGG | TCA | TCC | ATC | CGC | CTG | TGG | ACA | AGC | CCC | ACC | TTC | CAG |
| ----- | | | | | | | | | | | | | | | | | |
| V | R | P | S | Q | W | S | S | I | R | L | W | T | S | P | T | F | Q |
| ----- | | | | | | | | | | | | | | | | | |
| 1359 | | | | 1368 | | | 1377 | | | 1386 | | | 1395 | | | 1404 | |
| TGG | CTG | ATC | CCC | GAC | AGC | GCT | GAC | ACC | ACA | GCT | ACA | CCC | ACG | CAC | TGT | GCC | TAT |
| ----- | | | | | | | | | | | | | | | | | |
| W | L | I | P | D | S | A | D | T | T | A | T | P | T | H | C | A | Y |
| ----- | | | | | | | | | | | | | | | | | |
| 1413 | | | | 1422 | | | 1431 | | | 1440 | | | 1449 | | | 1458 | |
| GAC | AGG | ATC | GTG | GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT | GTT | CCC | GAC | TCG |
| ----- | | | | | | | | | | | | | | | | | |
| D | R | I | V | V | A | G | M | L | L | R | G | A | V | V | P | D | S |
| ----- | | | | | | | | | | | | | | | | | |
| 1467 | | | | 1476 | | | 1485 | | | 1494 | | | 1503 | | | 1512 | |
| GCT | CTT | CCC | TTT | AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC | CAA | CTG | GCC | CAA |
| ----- | | | | | | | | | | | | | | | | | |
| A | L | P | F | N | F | Q | A | A | Y | G | L | S | D | Q | L | A | Q |
| ----- | | | | | | | | | | | | | | | | | |
| 1521 | | | | 1530 | | | 1539 | | | 1548 | | | 1557 | | | 1566 | |
| GCC | ATC | AGT | GAC | CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | GGG | GGC | GGA | CCC | AAA |
| ----- | | | | | | | | | | | | | | | | | |
| A | I | S | D | H | Y | P | V | E | V | M | L | K | <u>G</u> | <u>G</u> | <u>G</u> | <u>P</u> | <u>K</u> |
| ----- | | | | | | | | | | | | | | | | | |
| 1575 | | | | 1584 | | | | | | | | | | | | | |
| AAG | AAG | CGC | AAG | GTT | TGA | 3' | | | | | | | | | | | |
| ----- | | | | | | | | | | | | | | | | | |
| <u>K</u> | <u>K</u> | <u>R</u> | <u>K</u> | <u>V</u> | * | | | | | | | | | | | | |

FIGURE 7

(A) pAS34

LOCUS PAS34.DNA 2196 bp 2196 bp 2196 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 34
 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file)
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS79 and AS80
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 501 a 677 c 607 g 411 t
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGAATACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCT AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAAGTGG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCAGACAG GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

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|----|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|--|
| | 9 | | | | 18 | | | | 27 | | | | 36 | | | | 45 | | | | 54 | |
| 5' | ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TTC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | GTC | CAC | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | M | G | W | S | C | I | I | L | F | L | V | A | T | A | T | G | V | H | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 63 | | | | 72 | | | | 81 | | | | 90 | | | | 99 | | | | 108 | |
| | TCC | CAG | GTG | CAG | CTG | GTG | CAG | TCT | GGG | GCA | GAG | GTG | AAA | AAG | CCT | GGG | GCC | TCA | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | <u>S</u> | Q | V | Q | L | V | Q | S | G | A | E | V | K | K | P | G | A | S | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 117 | | | | 126 | | | | 135 | | | | 144 | | | | 153 | | | | 162 | |
| | GTG | AAG | GTG | TCC | TGC | AAG | GCT | TCT | GGC | TAC | ACC | TTC | AGT | GCC | TAC | TGG | ATA | GAG | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | V | K | V | S | C | K | A | S | G | Y | T | F | S | A | Y | W | I | E | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 171 | | | | 180 | | | | 189 | | | | 198 | | | | 207 | | | | 216 | |
| | TGG | GTG | CGC | CAG | GCT | CCA | GGA | AAG | GGC | CTC | GAG | TGG | GTC | GGA | GAG | ATT | TTA | CCT | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | W | V | R | Q | A | P | G | K | G | L | E | W | V | G | E | I | L | P | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 225 | | | | 234 | | | | 243 | | | | 252 | | | | 261 | | | | 270 | |
| | GGA | AGT | AAT | AAT | TCT | AGA | TAC | AAT | GAG | AAG | TTC | AAG | GGC | CGA | GTG | ACA | GTC | ACT | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | G | S | N | N | S | R | Y | N | E | K | F | K | G | R | V | T | V | T | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 279 | | | | 288 | | | | 297 | | | | 306 | | | | 315 | | | | 324 | |
| | AGA | GAC | ACA | TCC | ACA | AAC | ACA | GCC | TAC | ATG | GAG | CTC | AGC | AGC | CTG | AGG | TCT | GAG | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | R | D | T | S | T | N | T | A | Y | M | E | L | S | S | L | R | S | E | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 333 | | | | 342 | | | | 351 | | | | 360 | | | | 369 | | | | 378 | |
| | GAC | ACA | GCC | GTC | TAT | TAC | TGT | GCA | AGA | TCC | TAC | GAC | TTT | GCC | TGG | TTT | GCT | TAC | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | D | T | A | V | Y | Y | C | A | R | S | Y | D | F | A | W | F | A | Y | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 387 | | | | 396 | | | | 405 | | | | 414 | | | | 423 | | | | 432 | |
| | TGG | GGC | CAA | GGG | ACT | CTG | GTC | ACA | GTC | TCC | TCA | GCC | TCC | ACC | AAG | GGC | CCA | TCG | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | W | G | Q | G | T | L | V | T | V | S | S | A | S | T | K | G | P | S | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 441 | | | | 450 | | | | 459 | | | | 468 | | | | 477 | | | | 486 | |
| | GTC | TTC | CCC | CTG | GCA | CCC | TCC | TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | V | F | P | L | A | P | S | S | K | S | T | S | G | G | T | A | A | L | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 495 | | | | 504 | | | | 513 | | | | 522 | | | | 531 | | | | 540 | |
| | GGC | TGC | CTG | GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | G | C | L | V | K | D | Y | F | P | E | P | V | T | V | S | W | N | S | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 549 | | | | 558 | | | | 567 | | | | 576 | | | | 585 | | | | 594 | |
| | GGC | GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | G | A | L | T | S | G | V | H | T | F | P | A | V | L | Q | S | S | G | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 603 | | | | 612 | | | | 621 | | | | 630 | | | | 639 | | | | 648 | |
| | CTC | TAC | TCC | CTC | AGC | AGC | GTG | GTG | ACC | GTG | CCC | TCC | AGC | AGC | TTG | GGC | ACC | CAG | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | L | Y | S | L | S | S | V | V | T | V | P | S | S | S | L | G | T | Q | | | | |
| | ----- | | | | | | | | | | | | | | | | | | | | | |
| | 657 | | | | 666 | | | | 675 | | | | 684 | | | | 693 | | | | 702 | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ACC | TAC | ATC | TGC | AAC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | AAG | GTG | GAC | AAG | AAA |
| T | Y | I | C | | V | N | H | K | P | S | N | T | K | V | D | K | K |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|-----|
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT | TGT GAC AAA ACT | CAC ACA TGC | CCA CCG TGC | CCA GCA CCT | |
| V E P K S | C D K T | H T C P | P C P A | P | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|-----|
| 765 | 774 | 783 | 792 | 801 | 810 |
| GAA CTC CTG GGG GGA | CCG TCA GTC TTC | CTC TTC CCC | CCA AAA CCC | AAG GAC ACC | |
| E L L G G | P S V F | L F P P | K P K D | T | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|-----|
| 819 | 828 | 837 | 846 | 855 | 864 |
| CTC ATG ATC TCC CGG | ACC CCT GAG GTC | ACA TGC GTG | GTG GTG GAC | GTG AGC CAC | |
| L M I S R | T P E V | T C V V | V D V S | H | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|-----|
| 873 | 882 | 891 | 900 | 909 | 918 |
| GAA GAC CCT GAG GTC | AAG TTC AAC TGG | TAC GTG GAC | GGC GTG GAG | GTG CAT AAT | |
| E D P E V | K F N W | Y V D G | V E V H | N | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|-----|
| 927 | 936 | 945 | 954 | 963 | 972 |
| GCC AAG ACA AAG CCG | CGG GAG GAG CAG | TAC AAC AGC | ACG TAC CGT | GTG GTC AGC | |
| A K T K P | R E E Q | Y N S T | Y R V V | S | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|------|
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| GTC CTC ACC GTC CTG | CAC CAG GAC TGG | CTG AAT GGC | AAG GAG TAC | AAG TGC AAG | |
| V L T V L | H Q D W | L N G K | E Y K C | K | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| GTC TCC AAC AAA GCC | CTC CCA GCC CCC | ATC GAG AAA ACC | ATC TCC AAA GCC | AAA | |
| V S N K A | L P A P | I E K T | I S K A | K | |

| | | | | | |
|---------------------|-----------------|-----------------|-------------|---------|------|
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| GGG CAG CCC CGA GAA | CCA CAG GTG TAC | ACC CTG CCC CCA | TCC CGG GAT | GAG CTG | |
| G Q P R E | P Q V Y | T L P P | S R D E | L | |

| | | | | | |
|---------------------|-----------------|-----------------|-------------|---------|------|
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| ACC AAG AAC CAG GTC | AGC CTG ACC TGC | CTG GTC AAA GGC | TTC TAT CCC | AGC GAC | |
| T K N Q V | S L T C | L V K G | F Y P S | D | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|------|
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |
| ATC GCC GTG GAG TGG | GAG AGC AAT GGG | CAG CCG GAG | AAC AAC TAC | AAG ACC ACG | |
| I A V E W | E S N G | Q P E N | N Y K T | T | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|------|
| 1251 | 1260 | 1269 | 1278 | 1287 | 1296 |
| CCT CCC GTG CTG GAC | TCC GAC GGC TCC | TTC TTC CTC | TAC AGC AAG | CTC ACC GTG | |
| P P V L D | S D G S | F F L Y | S K L T | V | |

| | | | | | |
|---------------------|-----------------|-------------|-------------|-------------|------|
| 1305 | 1314 | 1323 | 1332 | 1341 | 1350 |
| GAC AAG AGC AGG TGG | CAG CAG GGG AAC | GTC TTC TCA | TGC TCC GTG | ATG CAT GAG | |
| D K S R W | Q Q G N | V F S C | S V M H | E | |

| | | | | | |
|-----------------|-----------------|-------------------|-----------------|-------------|----------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| GCT CTG CAC AAG | TAC ACG CAG AAG | AGC CTC TCC CTG T | CG GGT AAA GGG | | |
| A L H N | H Y T Q | K S L S | L S P G | K | <u>G</u> |
| ----- | | | | | |
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| AGC GGC GGG CTG | AAG ATC GCA GCC | TTC AAC ATC CAG | ACA TTT GGG GAG | ACC AAG | |
| <u>S G G</u> | L K I A | A F N I | Q T F G | E T | K |
| ----- | | | | | |
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| ATG TCC AAT GCC | ACC CTC GTC AGC | TAC ATT GTG CAG | ATC CTG AGC CGC | TAC GAC | |
| M S N A | T L V S | Y I V Q | I L S R | Y D | |
| ----- | | | | | |
| 1521 | 1530 | 1539 | 1548 | 1557 | 1566 |
| ATC GCC CTG GTC | CAG GAG GTC AGA | GAC AGC CAC CTG | ACT GCC GTG GGG | AAG CTG | |
| I A L V | Q E V R | D S H L | T A V G | K L | |
| ----- | | | | | |
| 1575 | 1584 | 1593 | 1602 | 1611 | 1620 |
| CTG GAC AAC CTC | AAT CAG GAC GCA | CCA GAC ACC TAT | CAC TAC GTG GTC | AGT GAG | |
| L D N L | N Q D A | P D T Y | H Y V V | S E | |
| ----- | | | | | |
| 1629 | 1638 | 1647 | 1656 | 1665 | 1674 |
| CCA CTG GGA CGG | AAC AGC TAT AAG | GAG CGC TAC CTG | TTC GTG TAC AGG | CCT GAC | |
| P L G R | N S Y K | E R Y L | F V Y R | P D | |
| ----- | | | | | |
| 1683 | 1692 | 1701 | 1710 | 1719 | 1728 |
| CAG GTG TCT GCG | GTG GAC AGC TAC | TAC TAC TAC GAT | GAT GGC TGC GAG | CCC TGC GGG | |
| Q V S A | V D S Y | Y Y Y D | D G C E | P C G | |
| ----- | | | | | |
| 1737 | 1746 | 1755 | 1764 | 1773 | 1782 |
| AAC GAC ACC TTC | AAC CGA GAG CCA | GCC ATT GTC AGG | TTC TTC TCC CGG | TTC ACA | |
| N D T F | N R E P | A I V R | F F S R | F T | |
| ----- | | | | | |
| 1791 | 1800 | 1809 | 1818 | 1827 | 1836 |
| GAG GTC AGG GAG | TTT GCC ATT GTT | CCC CTG CAT GCG | GCC CCG GGG GAC | GCA GTA | |
| E V R E | F A I V | P L H A | A P G D | A V | |
| ----- | | | | | |
| 1845 | 1854 | 1863 | 1872 | 1881 | 1890 |
| GCC GAG ATC GAC | GCT CTC TAT GAC | GTC TAC CTG GAT | GTC CAA GAG AAA | TGG GGC | |
| A E I D | A L Y D | V Y L D | V Q E K | W G | |
| ----- | | | | | |
| 1899 | 1908 | 1917 | 1926 | 1935 | 1944 |
| TTG GAG GAC GTC | ATG TTG ATG GGC | GAC TTC AAT GCG | GGC TGC AGC TAT | GTG AGA | |
| L E D V | M L M G | D F N A | G C S Y | V R | |
| ----- | | | | | |
| 1953 | 1962 | 1971 | 1980 | 1989 | 1998 |
| CCC TCC CAG TGG | TCA TCC ATC CGC | CTG TGG ACA AGC | CCC ACC TTC CAG | TGG CTG | |
| P S Q W | S S I R | L W T S | P T F Q | W L | |
| ----- | | | | | |
| 2007 | 2016 | 2025 | 2034 | 2043 | 2052 |
| ATC CCC GAC AGC | GCT GAC ACC ACA | GCT ACA CCC ACG | CAC TGT GCC TAT | GAC AGG | |
| I P D S | A D T T | A T P T | H C A Y | D R | |

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|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|------|------|--|
| | | 2061 | | | 070 | | | 2079 | | | 2088 | | | 7 | | 2106 | | |
| ATC | GTG | GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT | GTT | CCC | BAC | TCG | GCT | CTT | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |
| I | V | V | A | G | M | L | L | R | G | A | V | V | P | D | S | A | L | |
| | | | | | | | | | | | | | | | | | | |
| | | 2115 | | | 2124 | | | 2133 | | | 2142 | | | 2151 | | | 2160 | |
| CCC | TTT | AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC | CAA | CTG | GCC | CAA | GCC | ATC | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |
| P | F | N | F | Q | A | A | Y | G | L | S | D | Q | L | A | Q | A | I | |
| | | | | | | | | | | | | | | | | | | |
| | | 2169 | | | 2178 | | | 2187 | | | 2196 | | | | | | | |
| AGT | GAC | CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | TGA | 3' | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | | | |
| S | D | H | Y | P | V | E | V | M | L | K | * | | | | | | | |

(A) pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 35
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS81 and AS82
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
 SITES Note
 BASE COUNT 500 a 677 c 606 g 410 t
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTIONTTC CCCGAACCGG TGACGGGTGTC GTGGAACCTA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAGGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTTCGTG ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT
1801 GTTCCCCTGC ATGCGGCCCC GGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

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FIGURE 8(B)

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ACC | TAC | ATC | TGC | ACC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | AAA | GTG | GAC | AAG | AAA |
| T | Y | I | C | N | V | N | H | K | P | S | N | T | K | V | D | K | K |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|-----|-----|
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT | TGT GAC AAA ACT | CAC ACA TGC CCA | CCG TGC CCA GCA | CCT | |
| V E P K S | C D K T H | T C P P C | P A P | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|-----|-----|
| 765 | 774 | 783 | 792 | 801 | 810 |
| GAA CTC CTG GGG GGA | CCG TCA GTC TTC | CTC TTC CCC CCA | AAA CCC AAG GAC | ACC | |
| E L L G G | P S V F L | F P P K P | K D T | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|-----|-----|
| 819 | 828 | 837 | 846 | 855 | 864 |
| CTC ATG ATC TCC CGG | ACC CCT GAG GTC | ACA TGC GTG GTG | GAC GTG AGC CAC | | |
| L M I S R | T P E V T | C V V V D | V S H | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|-----|-----|
| 873 | 882 | 891 | 900 | 909 | 918 |
| GAA GAC CCT GAG GTC | AAG TTC AAC TGG | TAC GTG GAC GGC | GTG GAG GTG CAT | AAT | |
| E D P E V | K F N W Y | V D G V E | V H N | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|-----|-----|
| 927 | 936 | 945 | 954 | 963 | 972 |
| GCC AAG ACA AAG CCG | CGG GAG GAG CAG | TAC AAC AGC ACG | TAC CGT GTG GTC | AGC | |
| A K T K P | R E E Q Y | N S T Y R | V V S | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| GTC CTC ACC GTC CTG | CAC CAG GAC TGG | CTG AAT GGC AAG | GAG TAC AAG TGC | AAG | |
| V L T V L | H Q D W L | N G K E Y | K C K | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| GTC TCC AAC AAA GCC | CTC CCA GCC CCC | ATC GAG AAA ACC | ATC TCC AAA GCC | AAA | |
| V S N K A | L P A P I | E K T I S | K A K | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| GGG CAG CCC CGA GAA | CCA CAG GTG TAC | ACC CTG CCC CCA | TCC CGG GAT GAG | CTG | |
| G Q P R E | P Q V Y T | L P P S R | D E L | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| ACC AAG AAC CAG GTC | AGC CTG ACC TGC | CTG GTC AAA GGC | TTC TAT CCC AGC | GAC | |
| T K N Q V | S L T C L | V K G F Y | P S D | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |
| ATC GCC GTG GAG TGG | GAG AGC AAT GGG | CAG CCG GAG AAC | AAC TAC AAG ACC | ACG | |
| I A V E W | E S N G Q | P E N N Y | K T T | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 1251 | 1260 | 1269 | 1278 | 1287 | 1296 |
| CCT CCC GTG CTG GAC | TCC GAC GGC TCC | TTC TTC CTC TAC | AGC AAG CTC ACC | GTG | |
| P P V L D | S D G S F | F L Y S K | L T V | | |

| | | | | | |
|---------------------|-----------------|-----------------|-----------------|------|------|
| 1305 | 1314 | 1323 | 1332 | 1341 | 1350 |
| GAC AAG AGC AGG TGG | CAG CAG GGG AAC | GTC TTC TCA TGC | TCC GTG ATG CAT | GAG | |
| D K S R W | Q Q G N V | F S C S V | M H E | | |

| | | | | | |
|---|---------------------------------|---------------------------------|-----------------|----------|----------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| GCT CTG CAC AAC | TAC ACG CAG AAG AGC CTC TCC CTG | TCG | TGG AAG GGG AGC | | |
| A L H N | H Y T Q K S L S L S | P | K | <u>G</u> | <u>S</u> |
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG | | | | | |
| <u>G</u> | <u>G</u> | L K I A A F N I Q T F G E T K M | | | |
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC | | | | | |
| S N A T L V S Y I V Q I L S R Y D I | | | | | |
| 1521 | 1530 | 1539 | 1548 | 1557 | 1566 |
| GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG | | | | | |
| A L V Q E V R D S H L T A V G K L L | | | | | |
| 1575 | 1584 | 1593 | 1602 | 1611 | 1620 |
| GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA | | | | | |
| D N L N Q D A P D T Y H Y V V S E P | | | | | |
| 1629 | 1638 | 1647 | 1656 | 1665 | 1674 |
| CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG | | | | | |
| L G R N S Y K E R Y L F V Y R P D Q | | | | | |
| 1683 | 1692 | 1701 | 1710 | 1719 | 1728 |
| GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC | | | | | |
| V S A V D S Y Y Y D D G C E P C G N | | | | | |
| 1737 | 1746 | 1755 | 1764 | 1773 | 1782 |
| GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG | | | | | |
| D T F N R E P A I V R F F S R F T E | | | | | |
| 1791 | 1800 | 1809 | 1818 | 1827 | 1836 |
| GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC | | | | | |
| V R E F A I V P L H A A P G D A V A | | | | | |
| 1845 | 1854 | 1863 | 1872 | 1881 | 1890 |
| GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG | | | | | |
| E I D A L Y D V Y L D V Q E K W G L | | | | | |
| 1899 | 1908 | 1917 | 1926 | 1935 | 1944 |
| GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC | | | | | |
| E D V M L M G D F N A G C S Y V R P | | | | | |
| 1953 | 1962 | 1971 | 1980 | 1989 | 1998 |
| TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC | | | | | |
| S Q W S S I R L W T S P T F Q W L I | | | | | |
| 2007 | 2016 | 2025 | 2034 | 2043 | 2052 |
| CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC | | | | | |
| P D S A D T T A T P T H C A Y D R I | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|
| | | 2061 | | | 2070 | | | 2079 | | | 2088 | | | 2097 | | | 2106 |
| GTG | GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT | GTT | CCC | GAC | TCG | GCT | CTT | CCC |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| V | V | A | G | M | L | L | R | G | A | V | V | P | D | S | A | L | P |
| | | | | | | | | | | | | | | | | | |
| | | 2115 | | | 2124 | | | 2133 | | | 2142 | | | 2151 | | | 2160 |
| TTT | AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC | CAA | CTG | GCC | CAA | GCC | ATC | AGT |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| F | N | F | Q | A | A | Y | G | L | S | D | Q | L | A | Q | A | I | S |
| | | | | | | | | | | | | | | | | | |
| | | 2169 | | | 2178 | | | 2187 | | | | | | | | | |
| GAC | CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | TGA | 3' | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | | | |
| D | H | Y | P | V | E | V | M | L | K | * | | | | | | | |

(A) pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 36
 DEFINITION Clone 18.24.1 with residue 1392 T > C
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS83 and AS84
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES Residue 1392 T > C silent S to S mutation
 SITES Note
 BASE COUNT 498 a 678 c 605 g 409 t
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACAT ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAA TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGAAGTCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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FIGURE 9 (B)

1. The first part of the report discusses the importance of maintaining accurate records of all transactions, including sales, purchases, and expenses. It emphasizes the need for consistency and transparency in financial reporting.

2. The second part of the report provides a detailed analysis of the company's financial performance over the past year. It includes a breakdown of revenue by product line and a comparison of actual results against budgeted figures.

3. The third part of the report focuses on the company's cash flow and liquidity. It highlights the need to maintain sufficient cash reserves to cover operating expenses and potential future obligations.

4. The fourth part of the report discusses the company's debt management strategy. It outlines the terms of existing loans and provides recommendations for optimizing the debt structure to minimize interest costs.

5. The fifth part of the report addresses the company's tax compliance obligations. It reviews the current tax position and identifies opportunities for tax optimization within the bounds of the law.

6. The sixth part of the report provides a summary of the findings and conclusions. It reiterates the importance of ongoing financial monitoring and offers suggestions for areas where the company can improve its financial health.

| | | | | | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|------|-----|-----|-----|------|-----|-----|-----|------|-----|-----|-----|------|-----|--|--|------|--|
| ACC | TAC | ATC | TGC | AAC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | AAG | GTG | GAC | AAG | AAA | | | | |
| T | Y | I | C | N | V | N | H | K | P | S | N | T | K | V | D | K | K | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 711 | | | | 720 | | | | 729 | | | | 738 | | | | 747 | | | | 756 | |
| GTT | GAG | CCC | AAA | TCT | TGT | GAC | AAA | ACT | CAC | ACA | TGC | CCA | CCG | TGC | CCA | GCA | CCT | | | | |
| V | E | P | K | S | C | D | K | T | H | T | C | P | P | C | P | A | P | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 765 | | | | 774 | | | | 783 | | | | 792 | | | | 801 | | | | 810 | |
| GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC | CTC | TTC | CCC | CCA | AAA | CCC | AAG | GAC | ACC | | | | |
| E | L | L | G | G | P | S | V | F | L | F | P | P | K | P | K | D | T | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 819 | | | | 828 | | | | 837 | | | | 846 | | | | 855 | | | | 864 | |
| CTC | ATG | ATC | TCC | CGG | ACC | CCT | GAG | GTC | ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | | | | |
| L | M | I | S | R | T | P | E | V | T | C | V | V | V | D | V | S | H | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 873 | | | | 882 | | | | 891 | | | | 900 | | | | 909 | | | | 918 | |
| GAA | GAC | CCT | GAG | GTC | AAG | TTC | AAC | TGG | TAC | GTG | GAC | GGC | GTG | GAG | GTG | CAT | AAT | | | | |
| E | D | P | E | V | K | F | N | W | Y | V | D | G | V | E | V | H | N | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 927 | | | | 936 | | | | 945 | | | | 954 | | | | 963 | | | | 972 | |
| GCC | AAG | ACA | AAG | CCG | CGG | GAG | GAG | CAG | TAC | AAC | AGC | ACG | TAC | CGT | GTG | GTC | AGC | | | | |
| A | K | T | K | P | R | E | E | Q | Y | N | S | T | Y | R | V | V | S | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 981 | | | | 990 | | | | 999 | | | | 1008 | | | | 1017 | | | | 1026 | |
| GTC | CTC | ACC | GTC | CTG | CAC | CAG | GAC | TGG | CTG | AAT | GGC | AAG | GAG | TAC | AAG | TGC | AAG | | | | |
| V | L | T | V | L | H | Q | D | W | L | N | G | K | E | Y | K | C | K | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1035 | | | | 1044 | | | | 1053 | | | | 1062 | | | | 1071 | | | | 1080 | |
| GTC | TCC | AAC | AAA | GCC | CTC | CCA | GCC | CCC | ATC | GAG | AAA | ACC | ATC | TCC | AAA | GCC | AAA | | | | |
| V | S | N | K | A | L | P | A | P | I | E | K | T | I | S | K | A | K | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1089 | | | | 1098 | | | | 1107 | | | | 1116 | | | | 1125 | | | | 1134 | |
| GGG | CAG | CCC | CGA | GAA | CCA | CAG | GTG | TAC | ACC | CTG | CCC | CCA | TCC | CGG | GAT | GAG | CTG | | | | |
| G | Q | P | R | E | P | Q | V | Y | T | L | P | P | S | R | D | E | L | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1143 | | | | 1152 | | | | 1161 | | | | 1170 | | | | 1179 | | | | 1188 | |
| ACC | AAG | AAC | CAG | GTC | AGC | CTG | ACC | TGC | CTG | GTC | AAA | GGC | TTC | TAT | CCC | AGC | GAC | | | | |
| T | K | N | Q | V | S | L | T | C | L | V | K | G | F | Y | P | S | D | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1197 | | | | 1206 | | | | 1215 | | | | 1224 | | | | 1233 | | | | 1242 | |
| ATC | GCC | GTG | GAG | TGG | GAG | AGC | AAT | GGG | CAG | CCG | GAG | AAC | AAC | TAC | AAG | ACC | ACG | | | | |
| I | A | V | E | W | E | S | N | G | Q | P | E | N | N | Y | K | T | T | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1251 | | | | 1260 | | | | 1269 | | | | 1278 | | | | 1287 | | | | 1296 | |
| CCT | CCC | GTG | CTG | GAC | TCC | GAC | GGC | TCC | TTC | TTC | CTC | TAC | AGC | AAG | CTC | ACC | GTG | | | | |
| P | P | V | L | D | S | D | G | S | F | F | L | Y | S | K | L | T | V | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1305 | | | | 1314 | | | | 1323 | | | | 1332 | | | | 1341 | | | | 1350 | |
| GAC | AAG | AGC | AGG | TGG | CAG | CAG | GGG | AAC | GTC | TTC | TCA | TGC | TCC | GTG | ATG | CAT | GAG | | | | |
| D | K | S | R | W | Q | Q | G | N | V | F | S | C | S | V | M | H | E | | | | |

| | | | | | |
|---|------|------|------|------|------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC | | | | | |
| A L H N H Y T Q K S L S L S P <u>G S G</u> | | | | | |
| ----- | | | | | |
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC | | | | | |
| <u>G</u> L K I A A F N I Q T F G E T K M S | | | | | |
| ----- | | | | | |
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC | | | | | |
| N A T L V S Y I V Q I L S R Y D I A | | | | | |
| ----- | | | | | |
| 1521 | 1530 | 1539 | 1548 | 1557 | 1566 |
| CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC | | | | | |
| L V Q E V R D S H L T A V G K L L D | | | | | |
| ----- | | | | | |
| 1575 | 1584 | 1593 | 1602 | 1611 | 1620 |
| AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG | | | | | |
| N L N Q D A P D T Y H Y V V S E P L | | | | | |
| ----- | | | | | |
| 1629 | 1638 | 1647 | 1656 | 1665 | 1674 |
| GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG | | | | | |
| G R N S Y K E R Y L F V Y R P D Q V | | | | | |
| ----- | | | | | |
| 1683 | 1692 | 1701 | 1710 | 1719 | 1728 |
| TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC | | | | | |
| S A V D S Y Y Y D D G C E P C G N D | | | | | |
| ----- | | | | | |
| 1737 | 1746 | 1755 | 1764 | 1773 | 1782 |
| ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC | | | | | |
| T F N R E P A I V R F F S R F T E V | | | | | |
| ----- | | | | | |
| 1791 | 1800 | 1809 | 1818 | 1827 | 1836 |
| AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG | | | | | |
| R E F A I V P L H A A P G D A V A E | | | | | |
| ----- | | | | | |
| 1845 | 1854 | 1863 | 1872 | 1881 | 1890 |
| ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG | | | | | |
| I D A L Y D V Y L D V Q E K W G L E | | | | | |
| ----- | | | | | |
| 1899 | 1908 | 1917 | 1926 | 1935 | 1944 |
| GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC | | | | | |
| D V M L M G D F N A G C S Y V R P S | | | | | |
| ----- | | | | | |
| 1953 | 1962 | 1971 | 1980 | 1989 | 1998 |
| CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC | | | | | |
| Q W S S I R L W T S P T F Q W L I P | | | | | |
| ----- | | | | | |
| 2007 | 2016 | 2025 | 2034 | 2043 | 2052 |
| GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG | | | | | |
| D S A D T T A T P T H C A Y D R I V | | | | | |

| | | | | | | | | | | | | | | | | | |
|------|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|
| | | 2061 | | | 2070 | | | 2079 | | | 2088 | | | 2097 | | | 2106 |
| .GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT | GTT | CCC | GAC | TCG | GCT | CTT | CCC | TTT |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| V | A | G | M | L | L | R | G | A | V | V | P | D | S | A | L | P | F |
| | | | | | | | | | | | | | | | | | |
| | | 2115 | | | 2124 | | | 2133 | | | 2142 | | | 2151 | | | 2160 |
| AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC | CAA | CTG | GCC | CAA | GCC | ATC | AGT | GAC |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| N | F | Q | A | A | Y | G | L | S | D | Q | L | A | Q | A | I | S | D |
| | | | | | | | | | | | | | | | | | |
| | | 2169 | | | 2178 | | | 2187 | | | | | | | | | |
| CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | TGA | 3' | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| H | Y | P | V | E | V | M | L | K | * | | | | | | | | |

(A) pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 37
 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) plus NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS79 and AS80
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 511 a 683 c 619 g 413 t
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAA AAGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT GGCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGCG GACCCAAAAA GAAGCGCAAG
2221 GTTTGA

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↳ NLS

FIGURE 10 (B)

[illegible]

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|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|--|--|------|--|--|--|--|------|
| ACC | TAC | ATC | TGC | ACC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | AAA | GTG | GAC | AAG | AAA | | | | | | | | |
| T | Y | I | C | N | V | N | H | K | P | S | N | T | K | V | D | K | K | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 711 | | | | | 720 | | | | | 729 | | | | | 738 | | | | | 747 | | | | | 756 |
| GTT | GAG | CCC | AAA | TCT | TGT | GAC | AAA | ACT | CAC | ACA | TGC | CCA | CCG | TGC | CCA | GCA | CCT | | | | | | | | |
| V | E | P | K | S | C | D | K | T | H | T | C | P | P | C | P | A | P | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 765 | | | | | 774 | | | | | 783 | | | | | 792 | | | | | 801 | | | | | 810 |
| GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC | CTC | TTC | CCC | CCA | AAA | CCC | AAG | GAC | ACC | | | | | | | | |
| E | L | L | G | G | P | S | V | F | L | F | P | P | K | P | K | D | T | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 819 | | | | | 828 | | | | | 837 | | | | | 846 | | | | | 855 | | | | | 864 |
| CTC | ATG | ATC | TCC | CGG | ACC | CCT | GAG | GTC | ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | | | | | | | | |
| L | M | I | S | R | T | P | E | V | T | C | V | V | V | D | V | S | H | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 873 | | | | | 882 | | | | | 891 | | | | | 900 | | | | | 909 | | | | | 918 |
| GAA | GAC | CCT | GAG | GTC | AAG | TTC | AAC | TGG | TAC | GTG | GAC | GGC | GTG | GAG | GTG | CAT | AAT | | | | | | | | |
| E | D | P | E | V | K | F | N | W | Y | V | D | G | V | E | V | H | N | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 927 | | | | | 936 | | | | | 945 | | | | | 954 | | | | | 963 | | | | | 972 |
| GCC | AAG | ACA | AAG | CCG | CGG | GAG | GAG | CAG | TAC | AAC | AGC | ACG | TAC | CGT | GTG | GTC | AGC | | | | | | | | |
| A | K | T | K | P | R | E | E | Q | Y | N | S | T | Y | R | V | V | S | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 981 | | | | | 990 | | | | | 999 | | | | | 1008 | | | | | 1017 | | | | | 1026 |
| GTC | CTC | ACC | GTC | CTG | CAC | CAG | GAC | TGG | CTG | AAT | GGC | AAG | GAG | TAC | AAG | TGC | AAG | | | | | | | | |
| V | L | T | V | L | H | Q | D | W | L | N | G | K | E | Y | K | C | K | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1035 | | | | | 1044 | | | | | 1053 | | | | | 1062 | | | | | 1071 | | | | | 1080 |
| GTC | TCC | AAC | AAA | GCC | CTC | CCA | GCC | CCC | ATC | GAG | AAA | ACC | ATC | TCC | AAA | GCC | AAA | | | | | | | | |
| V | S | N | K | A | L | P | A | P | I | E | K | T | I | S | K | A | K | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1089 | | | | | 1098 | | | | | 1107 | | | | | 1116 | | | | | 1125 | | | | | 1134 |
| GGG | CAG | CCC | CGA | GAA | CCA | CAG | GTG | TAC | ACC | CTG | CCC | CCA | TCC | CGG | GAT | GAG | CTG | | | | | | | | |
| G | Q | P | R | E | P | Q | V | Y | T | L | P | P | S | R | D | E | L | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1143 | | | | | 1152 | | | | | 1161 | | | | | 1170 | | | | | 1179 | | | | | 1188 |
| ACC | AAG | AAC | CAG | GTC | AGC | CTG | ACC | TGC | CTG | GTC | AAA | GGC | TTC | TAT | CCC | AGC | GAC | | | | | | | | |
| T | K | N | Q | V | S | L | T | C | L | V | K | G | F | Y | P | S | D | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1197 | | | | | 1206 | | | | | 1215 | | | | | 1224 | | | | | 1233 | | | | | 1242 |
| ATC | GCC | GTG | GAG | TGG | GAG | AGC | AAT | GGG | CAG | CCG | GAG | AAC | AAC | TAC | AAG | ACC | ACG | | | | | | | | |
| I | A | V | E | W | E | S | N | G | Q | P | E | N | N | Y | K | T | T | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1251 | | | | | 1260 | | | | | 1269 | | | | | 1278 | | | | | 1287 | | | | | 1296 |
| CCT | CCC | GTG | CTG | GAC | TCC | GAC | GGC | TCC | TTC | TTC | CTC | TAC | AGC | AAG | CTC | ACC | GTG | | | | | | | | |
| P | P | V | L | D | S | D | G | S | F | F | L | Y | S | K | L | T | V | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1305 | | | | | 1314 | | | | | 1323 | | | | | 1332 | | | | | 1341 | | | | | 1350 |
| GAC | AAG | AGC | AGG | TGG | CAG | CAG | GGG | AAC | GTC | TTC | TCA | TGC | TCC | GTG | ATG | CAT | GAG | | | | | | | | |
| D | K | S | R | W | Q | Q | G | N | V | F | S | C | S | V | M | H | E | | | | | | | | |

| | | | | | |
|---|------|------|------|------|------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG | | | | | |
| A L H N H Y T Q K S L S L S P G K <u>G</u> | | | | | |
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG | | | | | |
| <u>S G G</u> L K I A A F N I Q T F G E T K | | | | | |
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC | | | | | |
| M S N A T L V S Y I V Q I L S R Y D | | | | | |
| 1521 | 1530 | 1539 | 1548 | 1557 | 1566 |
| ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG | | | | | |
| I A L V Q E V R D S H L T A V G K L | | | | | |
| 1575 | 1584 | 1593 | 1602 | 1611 | 1620 |
| CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG | | | | | |
| L D N L N Q D A P D T Y H Y V V S E | | | | | |
| 1629 | 1638 | 1647 | 1656 | 1665 | 1674 |
| CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC | | | | | |
| P L G R N S Y K E R Y L F V Y R P D | | | | | |
| 1683 | 1692 | 1701 | 1710 | 1719 | 1728 |
| CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG | | | | | |
| Q V S A V D S Y Y Y D D G C E P C G | | | | | |
| 1737 | 1746 | 1755 | 1764 | 1773 | 1782 |
| AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA | | | | | |
| N D T F N R E P A I V R F F S R F T | | | | | |
| 1791 | 1800 | 1809 | 1818 | 1827 | 1836 |
| GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA | | | | | |
| E V R E F A I V P L H A A P G D A V | | | | | |
| 1845 | 1854 | 1863 | 1872 | 1881 | 1890 |
| GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC | | | | | |
| A E I D A L Y D V Y L D V Q E K W G | | | | | |
| 1899 | 1908 | 1917 | 1926 | 1935 | 1944 |
| TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA | | | | | |
| L E D V M L M G D F N A G C S Y V R | | | | | |
| 1953 | 1962 | 1971 | 1980 | 1989 | 1998 |
| CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG | | | | | |
| P S Q W S S I R L W T S P T F Q W L | | | | | |
| 2007 | 2016 | 2025 | 2034 | 2043 | 2052 |
| ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG | | | | | |
| I P D S A D T T A T P T H C A Y D R | | | | | |

| | | | | | |
|---|------|------|------|------|------|
| 2061 | 2070 | 2079 | 2088 | 2097 | 2106 |
| ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT | | | | | |
| I V V A G M L L R G A V V P D S A L | | | | | |

| | | | | | |
|---|------|------|------|------|------|
| 2115 | 2124 | 2133 | 2142 | 2151 | 2160 |
| CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC | | | | | |
| P F N F Q A A Y G L S D Q L A Q A I | | | | | |

| | | | | | |
|---|------|------|------|------|------|
| 2169 | 2178 | 2187 | 2196 | 2205 | 2214 |
| AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG | | | | | |
| S D H Y P V E V M L K <u>G G G P K K K</u> | | | | | |

| |
|--------------------|
| 2223 |
| CGC AAG GTT TGA 3' |
| <u>R K V</u> * |

(A) pAS38

LOCUS PAS38.DNA 2223 bp 2193 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 38
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS81 and AS82
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
 SITES Note
 BASE COUNT 510 a 683 c 618 g 412 t
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGTC GTGGAACCTA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTGAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAA TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAGGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT
1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGCGGAC CCAAAAGAA GCGCAAGGTT
2221 TGA

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L3 NLS

FIGURE 11 (B)

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |

| | | | | | | | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|------|-----|-----|-----|------|-----|-----|-----|------|-----|-----|-----|------|-----|--|--|------|--|--|--|
| ACC | TAC | ATC | TGC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | ATG | GAC | AAG | AAA | | | | | | | | |
| T | Y | I | C | N | V | N | H | K | P | S | N | T | K | V | D | | | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 711 | | | | 720 | | | | 729 | | | | 738 | | | | 747 | | | | 756 | | | |
| GTT | GAG | CCC | AAA | TCT | TGT | GAC | AAA | ACT | CAC | ACA | TGC | CCA | CCG | TGC | CCA | GCA | CCT | | | | | | |
| V | E | P | K | S | C | D | K | T | H | T | C | P | P | C | P | A | P | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 765 | | | | 774 | | | | 783 | | | | 792 | | | | 801 | | | | 810 | | | |
| GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC | CTC | TTC | CCC | CCA | AAA | CCC | AAG | GAC | ACC | | | | | | |
| E | L | L | G | G | P | S | V | F | L | F | P | P | K | P | K | D | T | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 819 | | | | 828 | | | | 837 | | | | 846 | | | | 855 | | | | 864 | | | |
| CTC | ATG | ATC | TCC | CGG | ACC | CCT | GAG | GTC | ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | | | | | | |
| L | M | I | S | R | T | P | E | V | T | C | V | V | V | D | V | S | H | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 873 | | | | 882 | | | | 891 | | | | 900 | | | | 909 | | | | 918 | | | |
| GAA | GAC | CCT | GAG | GTC | AAG | TTC | AAC | TGG | TAC | GTG | GAC | GGC | GTG | GAG | GTG | CAT | AAT | | | | | | |
| E | D | P | E | V | K | F | N | W | Y | V | D | G | V | E | V | H | N | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 927 | | | | 936 | | | | 945 | | | | 954 | | | | 963 | | | | 972 | | | |
| GCC | AAG | ACA | AAG | CCG | CGG | GAG | GAG | CAG | TAC | AAC | AGC | ACG | TAC | CGT | GTG | GTC | AGC | | | | | | |
| A | K | T | K | P | R | E | E | Q | Y | N | S | T | Y | R | V | V | S | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 981 | | | | 990 | | | | 999 | | | | 1008 | | | | 1017 | | | | 1026 | | | |
| GTC | CTC | ACC | GTC | CTG | CAC | CAG | GAC | TGG | CTG | AAT | GGC | AAG | GAG | TAC | AAG | TGC | AAG | | | | | | |
| V | L | T | V | L | H | Q | D | W | L | N | G | K | E | Y | K | C | K | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 1035 | | | | 1044 | | | | 1053 | | | | 1062 | | | | 1071 | | | | 1080 | | | |
| GTC | TCC | AAC | AAA | GCC | CTC | CCA | GCC | CCC | ATC | GAG | AAA | ACC | ATC | TCC | AAA | GCC | AAA | | | | | | |
| V | S | N | K | A | L | P | A | P | I | E | K | T | I | S | K | A | K | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 1089 | | | | 1098 | | | | 1107 | | | | 1116 | | | | 1125 | | | | 1134 | | | |
| GGG | CAG | CCC | CGA | GAA | CCA | CAG | GTG | TAC | ACC | CTG | CCC | CCA | TCC | CGG | GAT | GAG | CTG | | | | | | |
| G | Q | P | R | E | P | Q | V | Y | T | L | P | P | S | R | D | E | L | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 1143 | | | | 1152 | | | | 1161 | | | | 1170 | | | | 1179 | | | | 1188 | | | |
| ACC | AAG | AAC | CAG | GTC | AGC | CTG | ACC | TGC | CTG | GTC | AAA | GGC | TTC | TAT | CCC | AGC | GAC | | | | | | |
| T | K | N | Q | V | S | L | T | C | L | V | K | G | F | Y | P | S | D | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 1197 | | | | 1206 | | | | 1215 | | | | 1224 | | | | 1233 | | | | 1242 | | | |
| ATC | GCC | GTG | GAG | TGG | GAG | AGC | AAT | GGG | CAG | CCG | GAG | AAC | AAC | TAC | AAG | ACC | ACG | | | | | | |
| I | A | V | E | W | E | S | N | G | Q | P | E | N | N | Y | K | T | T | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 1251 | | | | 1260 | | | | 1269 | | | | 1278 | | | | 1287 | | | | 1296 | | | |
| CCT | CCC | GTG | CTG | GAC | TCC | GAC | GGC | TCC | TTC | TTC | CTC | TAC | AGC | AAG | CTC | ACC | GTG | | | | | | |
| P | P | V | L | D | S | D | G | S | F | F | L | Y | S | K | L | T | V | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | | | |
| 1305 | | | | 1314 | | | | 1323 | | | | 1332 | | | | 1341 | | | | 1350 | | | |
| GAC | AAG | AGC | AGG | TGG | CAG | CAG | GGG | AAC | GTC | TTC | TCA | TGC | TCC | GTG | ATG | CAT | GAG | | | | | | |
| D | K | S | R | W | Q | Q | G | N | V | F | S | C | S | V | M | H | E | | | | | | |

| | | | | | |
|---|------|------|------|------|------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC | | | | | |
| A L H N H Y T Q K S L S L S P K <u>G S</u> | | | | | |
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG | | | | | |
| <u>G G</u> L K I A A F N I Q T F G E T K M | | | | | |
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC | | | | | |
| S N A T L V S Y I V Q I L S R Y D I | | | | | |
| 1521 | 1530 | 1539 | 1548 | 1557 | 1566 |
| GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG | | | | | |
| A L V Q E V R D S H L T A V G K L L | | | | | |
| 1575 | 1584 | 1593 | 1602 | 1611 | 1620 |
| GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA | | | | | |
| D N L N Q D A P D T Y H Y V V S E P | | | | | |
| 1629 | 1638 | 1647 | 1656 | 1665 | 1674 |
| CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG | | | | | |
| L G R N S Y K E R Y L F V Y R P D Q | | | | | |
| 1683 | 1692 | 1701 | 1710 | 1719 | 1728 |
| GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC | | | | | |
| V S A V D S Y Y Y D D G C E P C G N | | | | | |
| 1737 | 1746 | 1755 | 1764 | 1773 | 1782 |
| GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG | | | | | |
| D T F N R E P A I V R F F S R F T E | | | | | |
| 1791 | 1800 | 1809 | 1818 | 1827 | 1836 |
| GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC | | | | | |
| V R E F A I V P L H A A P G D A V A | | | | | |
| 1845 | 1854 | 1863 | 1872 | 1881 | 1890 |
| GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG | | | | | |
| E I D A L Y D V Y L D V Q E K W G L | | | | | |
| 1899 | 1908 | 1917 | 1926 | 1935 | 1944 |
| GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC | | | | | |
| E D V M L M G D F N A G C S Y V R P | | | | | |
| 1953 | 1962 | 1971 | 1980 | 1989 | 1998 |
| TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC | | | | | |
| S Q W S S I R L W T S P T F Q W L I | | | | | |
| 2007 | 2016 | 2025 | 2034 | 2043 | 2052 |
| CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC | | | | | |
| P D S A D T T A T P T H C A Y D R I | | | | | |

| | | | | | |
|-----------------|-----------------|-----------------|-----------------|---------|------|
| 2061 | 2070 | 2079 | 2088 | 2097 | 2106 |
| GTG GTT GCA GGG | ATG CTG CTC CGA | GGG GCC GTT GTT | CCC GAC TCG GCT | CTT CCC | |
| V V A G | M L L R | G A V V | P D S A | L P | |

| | | | | | |
|-----------------|-----------------|-----------------|-------------|-------------|------|
| 2115 | 2124 | 2133 | 2142 | 2151 | 2160 |
| TTT AAC TTC CAG | GCT GCC TAT GGC | CTG AGT GAC CAA | CTG GCC CAA | GCC ATC AGT | |
| F N F Q | A A Y G | L S D Q | L A Q A | I S | |

| | | | | | |
|-----------------|-----------------|-------------|----------------|--------------|----------|
| 2169 | 2178 | 2187 | 2196 | 2205 | 2214 |
| GAC CAC TAT CCA | GTG GAG GTG ATG | CTG AAG GGG | GGC GGA CCC | AAA AAG AAG | CGC |
| D H Y P | V E V M | L K | <u>G G G P</u> | <u>K K K</u> | <u>R</u> |

2223
AAG GTT TGA 3'

K V *

FIGURE 1

(4) pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 39
 DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS83 and AS84
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES Residue 1392 T > C silent S to S mutation
 SITES Note
 BASE COUNT 508 a 684 c 617 g 411 t
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTGAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAA TACAAGACCA CGCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGA CTGCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GCGGACCCA AAAAGAAGCG CAAGGTTTGA

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FIGURE 12(B)

1. The first group of people who are interested in the study of the history of the world are the people who are interested in the history of the world.

| | | | | | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|------|-----|-----|-----|------|-----|-----|-----|------|-----|-----|-----|------|-----|--|--|------|--|
| ACC | TAC | ATC | TG | | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | | TG | GAC | AAG | AAA | | | | |
| T | Y | I | C | N | V | N | H | K | P | S | N | T | K | V | D | K | K | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 711 | | | | 720 | | | | 729 | | | | 738 | | | | 747 | | | | 756 | |
| GTT | GAG | CCC | AAA | TCT | TGT | GAC | AAA | ACT | CAC | ACA | TGC | CCA | CCG | TGC | CCA | GCA | CCT | | | | |
| V | E | P | K | S | C | D | K | T | H | T | C | P | P | C | P | A | P | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 765 | | | | 774 | | | | 783 | | | | 792 | | | | 801 | | | | 810 | |
| GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC | CTC | TTC | CCC | CCA | AAA | CCC | AAG | GAC | ACC | | | | |
| E | L | L | G | G | P | S | V | F | L | F | P | P | K | P | K | D | T | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 819 | | | | 828 | | | | 837 | | | | 846 | | | | 855 | | | | 864 | |
| CTC | ATG | ATC | TCC | CGG | ACC | CCT | GAG | GTC | ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | | | | |
| L | M | I | S | R | T | P | E | V | T | C | V | V | V | D | V | S | H | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 873 | | | | 882 | | | | 891 | | | | 900 | | | | 909 | | | | 918 | |
| GAA | GAC | CCT | GAG | GTC | AAG | TTC | AAC | TGG | TAC | GTG | GAC | GGC | GTG | GAG | GTG | CAT | AAT | | | | |
| E | D | P | E | V | K | F | N | W | Y | V | D | G | V | E | V | H | N | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 927 | | | | 936 | | | | 945 | | | | 954 | | | | 963 | | | | 972 | |
| GCC | AAG | ACA | AAG | CCG | CGG | GAG | GAG | CAG | TAC | AAC | AGC | ACG | TAC | CGT | GTG | GTC | AGC | | | | |
| A | K | T | K | P | R | E | E | Q | Y | N | S | T | Y | R | V | V | S | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 981 | | | | 990 | | | | 999 | | | | 1008 | | | | 1017 | | | | 1026 | |
| GTC | CTC | ACC | GTC | CTG | CAC | CAG | GAC | TGG | CTG | AAT | GGC | AAG | GAG | TAC | AAG | TGC | AAG | | | | |
| V | L | T | V | L | H | Q | D | W | L | N | G | K | E | Y | K | C | K | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1035 | | | | 1044 | | | | 1053 | | | | 1062 | | | | 1071 | | | | 1080 | |
| GTC | TCC | AAC | AAA | GCC | CTC | CCA | GCC | CCC | ATC | GAG | AAA | ACC | ATC | TCC | AAA | GCC | AAA | | | | |
| V | S | N | K | A | L | P | A | P | I | E | K | T | I | S | K | A | K | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1089 | | | | 1098 | | | | 1107 | | | | 1116 | | | | 1125 | | | | 1134 | |
| GGG | CAG | CCC | CGA | GAA | CCA | CAG | GTG | TAC | ACC | CTG | CCC | CCA | TCC | CGG | GAT | GAG | CTG | | | | |
| G | Q | P | R | E | P | Q | V | Y | T | L | P | P | S | R | D | E | L | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1143 | | | | 1152 | | | | 1161 | | | | 1170 | | | | 1179 | | | | 1188 | |
| ACC | AAG | AAC | CAG | GTC | AGC | CTG | ACC | TGC | CTG | GTC | AAA | GGC | TTC | TAT | CCC | AGC | GAC | | | | |
| T | K | N | Q | V | S | L | T | C | L | V | K | G | F | Y | P | S | D | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1197 | | | | 1206 | | | | 1215 | | | | 1224 | | | | 1233 | | | | 1242 | |
| ATC | GCC | GTG | GAG | TGG | GAG | AGC | AAT | GGG | CAG | CCG | GAG | AAC | AAC | TAC | AAG | ACC | ACG | | | | |
| I | A | V | E | W | E | S | N | G | Q | P | E | N | N | Y | K | T | T | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1251 | | | | 1260 | | | | 1269 | | | | 1278 | | | | 1287 | | | | 1296 | |
| CCT | CCC | GTG | CTG | GAC | TCC | GAC | GGC | TCC | TTC | TTC | CTC | TAC | AGC | AAG | CTC | ACC | GTG | | | | |
| P | P | V | L | D | S | D | G | S | F | F | L | Y | S | K | L | T | V | | | | |
| ----- | | | | | | | | | | | | | | | | | | | | | |
| 1305 | | | | 1314 | | | | 1323 | | | | 1332 | | | | 1341 | | | | 1350 | |
| GAC | AAG | AGC | AGG | TGG | CAG | CAG | GGG | AAC | GTC | TTC | TCA | TGC | TCC | GTG | ATG | CAT | GAG | | | | |
| D | K | S | R | W | Q | Q | G | N | V | F | S | C | S | V | M | H | E | | | | |

| | | | | |
|---|--------------|------|------|------|
| 1359 | 68 | 1377 | 1386 | 1404 |
| GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC | GGG AGC GGC | | | |
| A L H N H Y T Q K S L S L S P | <u>G S G</u> | | | |
| 1413 | 1422 | 1431 | 1440 | 1449 |
| GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC | | | | |
| <u>G</u> L K I A A F N I Q T F G E T K M S | | | | |
| 1467 | 1476 | 1485 | 1494 | 1503 |
| AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC | | | | |
| N A T L V S Y I V Q I L S R Y D I A | | | | |
| 1521 | 1530 | 1539 | 1548 | 1557 |
| CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC | | | | |
| L V Q E V R D S H L T A V G K L L D | | | | |
| 1575 | 1584 | 1593 | 1602 | 1611 |
| AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG | | | | |
| N L N Q D A P D T Y H Y V V S E P L | | | | |
| 1629 | 1638 | 1647 | 1656 | 1665 |
| GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG | | | | |
| G R N S Y K E R Y L F V Y R P D Q V | | | | |
| 1683 | 1692 | 1701 | 1710 | 1719 |
| TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC | | | | |
| S A V D S Y Y Y D D G C E P C G N D | | | | |
| 1737 | 1746 | 1755 | 1764 | 1773 |
| ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC | | | | |
| T F N R E P A I V R F F S R F T E V | | | | |
| 1791 | 1800 | 1809 | 1818 | 1827 |
| AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG | | | | |
| R E F A I V P L H A A P G D A V A E | | | | |
| 1845 | 1854 | 1863 | 1872 | 1881 |
| ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG | | | | |
| I D A L Y D V Y L D V Q E K W G L E | | | | |
| 1899 | 1908 | 1917 | 1926 | 1935 |
| GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC | | | | |
| D V M L M G D F N A G C S Y V R P S | | | | |
| 1953 | 1962 | 1971 | 1980 | 1989 |
| CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC | | | | |
| Q W S S I R L W T S P T F Q W L I P | | | | |
| 2007 | 2016 | 2025 | 2034 | 2043 |
| GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG | | | | |
| D S A D T T A T P T H C A Y D R I V | | | | |

| | | | | | |
|---|------|------|------|------|------|
| 2061 | 2070 | 2079 | 2088 | 2097 | 2106 |
| GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT | | | | | |
| V A G M L L R G A V V P D S A L P F | | | | | |
| 2115 | 2124 | 2133 | 2142 | 2151 | 2160 |
| AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC | | | | | |
| N F Q A A Y G L S D Q L A Q A I S D | | | | | |
| 2169 | 2178 | 2187 | 2196 | 2205 | 2214 |
| CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC AAG | | | | | |
| H Y P V E V M L K G <u>G G P K K K R K</u> | | | | | |

GTT TGA 3'

V*

(A) pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 343 a 467 c 430 g 308 t
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
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901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
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1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

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LOCUS FDDNASE101 1548 BP SS-DNA SYN 25-AUG-2000
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
FEATURES Location/Qualifiers
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frag 721..780
/note="1 to 60 of 101/105linker"
frag join(721..>735,<736..>759,<760..>780)
/note="1 to 80 of 102linker [Split]"
BASE COUNT 343 A 465 C 431 G 309 T 0 OTHER
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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCGGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCGCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

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LOCUS FDDNASE101 1557 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 /note="1 to 1548 of PAS101.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 344 A 471 C 433 G 309 T 0 OTHER
 ORIGIN -

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61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG
541 TGGAATCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTG TG ACAAACCTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTGAGAGAC
901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCAGGGGA CGCAGTAGCC
1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
1501 GACCAACTGG CCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA

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FIGURE 13 (D)

55/113

| | | | | | |
|---|------|------|------|------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG | | | | | |
| L Y S L S S V V T V P S S S L G T Q | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA | | | | | |
| T Y I C N V N H K P S N T K V D K K | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT | | | | | |
| V E P K S C D K T H T C P P C P A P | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG | | | | | |
| E G G L K I A A F N I Q T F G E T K | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC | | | | | |
| M S N A T L V S Y I V Q I L S R Y D | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG | | | | | |
| I A L V Q E V R D S H L T A V G K L | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG | | | | | |
| L D N L N Q D A P D T Y H Y V V S E | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC | | | | | |
| P L G R N S Y K E R Y L F V Y R P D | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG | | | | | |
| Q V S A V D S Y Y Y D D G C E P C G | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA | | | | | |
| N D T F N R E P A I V R F F S R F T | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA | | | | | |
| E V R E F A I V P L H A A P G D A V | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|---|
| GCC | GAG | ATC | GAC | CTC | TAT | GAC | GTC | TAC | CTG | GAT | GTC | GAG | AAA | TGG | GGC | | |
| A | E | I | D | A | L | Y | D | V | Y | L | D | V | Q | E | K | W | G |

| | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1251 | 1260 | 1269 | 1278 | 1287 | 1296 | | | | | | | | | | | | |
| TTG | GAG | GAC | GTC | ATG | TTG | ATG | GGC | GAC | TTC | AAT | GCG | GGC | TGC | AGC | TAT | GTG | AGA |
| L | E | D | V | M | L | M | G | D | F | N | A | G | C | S | Y | V | R |

| | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1305 | 1314 | 1323 | 1332 | 1341 | 1350 | | | | | | | | | | | | |
| CCC | TCC | CAG | TGG | TCA | TCC | ATC | CGC | CTG | TGG | ACA | AGC | CCC | ACC | TTC | CAG | TGG | CTG |
| P | S | Q | W | S | S | I | R | L | W | T | S | P | T | F | Q | W | L |

| | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 | | | | | | | | | | | | |
| ATC | CCC | GAC | AGC | GCT | GAC | ACC | ACA | GCT | ACA | CCC | ACG | CAC | TGT | GCC | TAT | GAC | AGG |
| I | P | D | S | A | D | T | T | A | T | P | T | H | C | A | Y | D | R |

| | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 | | | | | | | | | | | | |
| ATC | GTG | GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT | GTT | CCC | GAC | TCG | GCT | CTT |
| I | V | V | A | G | M | L | L | R | G | A | V | V | P | D | S | A | L |

| | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 | | | | | | | | | | | | |
| CCC | TTT | AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC | CAA | CTG | GCC | CAA | GCC | ATC |
| P | F | N | F | Q | A | A | Y | G | L | S | D | Q | L | A | Q | A | I |

| | | | | | | | | | | | | |
|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|----|
| 1521 | 1530 | 1539 | 1548 | | | | | | | | | |
| AGT | GAC | CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | TGA | 3' |
| S | D | H | Y | P | V | E | V | M | L | K | * | |

FIGURE (A) pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna) (see Figure 2)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 345 a 469 c 440 g 312 t
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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
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181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
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901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAAGTTCCA GGCTGCCTAT
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1561 AAGTGA

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LOCUS FDDNASE102 1566 BP SS-DNA SYN 23-MAR-2001
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
BASE COUNT 345 A 468 C 440 G 313 T 0 OTHER
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181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
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361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGA TACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTGAGTGG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAG CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA

LOCUS FDDNASE302 1575 BP SS-DNA SYN 29-AUG-2000
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
FEATURES Location/Qualifiers
frag 10..1575
/note="1 to 1566 of FdDNase102correct"
BASE COUNT 346 A 474 C 442 G 313 T 0 OTHER
ORIGIN -

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61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
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361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG
541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
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781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
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1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
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File : PAS102.DNA
Range : 1 - 1566 Mode : Normal
Codon Table : Universal

FIGURE 14 (D)

| | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5' | ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TTC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | GTC | CAC |
| | M | G | W | S | C | I | I | L | F | L | V | A | T | A | T | G | V | H |
| | TCC | CAG | GTG | CAG | CTG | GTG | CAG | TCT | GGG | GCA | GAG | GTG | AAA | AAG | CCT | GGG | GCC | TCA |
| | S | Q | V | Q | L | V | Q | S | G | A | E | V | K | K | P | G | A | S |
| | GTG | AAG | GTG | TCC | TGC | AAG | GCT | TCT | GGC | TAC | ACC | TTC | AGT | GCC | TAC | TGG | ATA | GAG |
| | V | K | V | S | C | K | A | S | G | Y | T | F | S | A | Y | W | I | E |
| | TGG | GTG | CGC | CAG | GCT | CCA | GGA | AAG | GGC | CTC | GAG | TGG | GTC | GGA | GAG | ATT | TTA | CCT |
| | W | V | R | Q | A | P | G | K | G | L | E | W | V | G | E | I | L | P |
| | GGA | AGT | AAT | AAT | TCT | AGA | TAC | AAT | GAG | AAG | TTC | AAG | GGC | CGA | GTG | ACA | GTC | ACT |
| | G | S | N | N | S | R | Y | N | E | K | F | K | G | R | V | T | V | T |
| | AGA | GAC | ACA | TCC | ACA | AAC | ACA | GCC | TAC | ATG | GAG | CTC | AGC | AGC | CTG | AGG | TCT | GAG |
| | R | D | T | S | T | N | T | A | Y | M | E | L | S | S | L | R | S | E |
| | GAC | ACA | GCC | GTC | TAT | TAC | TGT | GCA | AGA | TCC | TAC | GAC | TTT | GCC | TGG | TTT | GCT | TAC |
| | D | T | A | V | Y | Y | C | A | R | S | Y | D | F | A | W | F | A | Y |
| | TGG | GGC | CAA | GGG | ACT | CTG | GTC | ACA | GTC | TCC | TCA | GCC | TCC | ACC | AAG | GGC | CCA | TCG |
| | W | G | Q | G | T | L | V | T | V | S | S | A | S | T | K | G | P | S |
| | GTC | TTC | CCC | CTG | GCA | CCC | TCC | TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG |
| | V | F | P | L | A | P | S | S | K | S | T | S | G | G | T | A | A | L |
| | GGC | TGC | CTG | GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA |
| | G | C | L | V | K | D | Y | F | P | E | P | V | T | V | S | W | N | S |
| | GGC | GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA |
| | G | A | L | T | S | G | V | H | T | F | P | A | V | L | Q | S | S | G |

| | | | | | |
|---|---|------|------|------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC AGC | AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG | | | | |
| L Y S L S S V V T V P S S S L G T Q | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA | | | | | |
| T Y I C N V N H K P S N T K V D K K | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG | | | | | |
| V E P K S C D K T H T C C V E C P P | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG | | | | | |
| C P A P E G S G G L K I A A F N I Q | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG | | | | | |
| T F G E T K M S N A T L V S Y I V Q | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG | | | | | |
| I L S R Y D I A L V Q E V R D S H L | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT | | | | | |
| T A V G K L L D N L N Q D A P D T Y | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG | | | | | |
| H Y V V S E P L G R N S Y K E R Y L | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT | | | | | |
| F V Y R P D Q V S A V D S Y Y Y D D | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG | | | | | |
| G C E P C G N D T F N R E P A I V R | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG | | | | | |
| F F S R F T E V R E F A I V P L H A | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

| | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|------|-----|--------|
| GCC | CCG | GGG | GAC | ATA | GTA | GCC | GAG | ATC | GAC | GCT | CTC | TAT | GTC | TAC | CTG | GAT | |
| ----- | | | | | | | | | | | | | | | | | |
| A | P | G | D | A | V | A | E | I | D | A | L | Y | D | V | Y | L | D |
| | | | | | | | | | | | | | | | | | |
| 1251 | | | | 1260 | | | 1269 | | | 1278 | | | 1287 | | 1296 | | |
| GTC | CAA | GAG | AAA | TGG | GGC | TTG | GAG | GAC | GTC | ATG | TTG | ATG | GGC | GAC | TTC | AAT | GCG |
| ----- | | | | | | | | | | | | | | | | | |
| V | Q | E | K | W | G | L | E | D | V | M | L | M | G | D | F | N | A |
| | | | | | | | | | | | | | | | | | |
| 1305 | | | | 1314 | | | 1323 | | | 1332 | | | 1341 | | 1350 | | |
| GGC | TGC | AGC | TAT | GTG | AGA | CCC | TCC | CAG | TGG | TCA | TCC | ATC | CGC | CTG | TGG | ACA | AGC |
| ----- | | | | | | | | | | | | | | | | | |
| G | C | S | Y | V | R | P | S | Q | W | S | S | I | R | L | W | T | S |
| | | | | | | | | | | | | | | | | | |
| 1359 | | | | 1368 | | | 1377 | | | 1386 | | | 1395 | | 1404 | | |
| CCC | ACC | TTC | CAG | TGG | CTG | ATC | CCC | GAC | AGC | GCT | GAC | ACC | ACA | GCT | ACA | CCC | ACG |
| ----- | | | | | | | | | | | | | | | | | |
| P | T | F | Q | W | L | I | P | D | S | A | D | T | T | A | T | P | T |
| | | | | | | | | | | | | | | | | | |
| 1413 | | | | 1422 | | | 1431 | | | 1440 | | | 1449 | | 1458 | | |
| CAC | TGT | GCC | TAT | GAC | AGG | ATC | GTG | GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT |
| ----- | | | | | | | | | | | | | | | | | |
| H | C | A | Y | D | R | I | V | V | A | G | M | L | L | R | G | A | V |
| | | | | | | | | | | | | | | | | | |
| 1467 | | | | 1476 | | | 1485 | | | 1494 | | | 1503 | | 1512 | | |
| GTT | CCC | GAC | TCG | GCT | CTT | CCC | TTT | AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC |
| ----- | | | | | | | | | | | | | | | | | |
| V | P | D | S | A | L | P | F | N | F | Q | A | A | Y | G | L | S | D |
| | | | | | | | | | | | | | | | | | |
| 1521 | | | | 1530 | | | 1539 | | | 1548 | | | 1557 | | 1566 | | |
| CAA | CTG | GCC | CAA | GCC | ATC | AGT | GAC | CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | TGA 3' |
| ----- | | | | | | | | | | | | | | | | | |
| Q | L | A | Q | A | I | S | D | H | Y | P | V | E | V | M | L | K | * |

(A) pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 344 a 468 c 436 g 312 t
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1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
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Figure 1S (B)

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DEFINITION   -
ACCESSION    -
KEYWORDS      -
SOURCE        -
FEATURES             Location/Qualifiers
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 ACCESSION -
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 SOURCE -
 FEATURES Location/Qualifiers
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 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 345 A 473 C 438 G 313 T 0 OTHER
 ORIGIN -

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181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
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1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
1321 TCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
1441 ATGCTGCTCC GAGGGGCCGT TGTTCCTGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
1561 CTGAAGTGA

```

File : PAS103.DNA
Range : 1 - 560 Mode : Normal
Codon Table : Universal

FIGURE 1S (D)

| | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5' | ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TTC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | GTC | CAC |
| | M | G | W | S | C | I | I | L | F | L | V | A | T | A | T | G | V | H |
| | TCC | CAG | GTG | CAG | CTG | GTG | CAG | TCT | GGG | GCA | GAG | GTG | AAA | AAG | CCT | GGG | GCC | TCA |
| | S | Q | V | Q | L | V | Q | S | G | A | E | V | K | K | P | G | A | S |
| | GTG | AAG | GTG | TCC | TGC | AAG | GCT | TCT | GGC | TAC | ACC | TTC | AGT | GCC | TAC | TGG | ATA | GAG |
| | V | K | V | S | C | K | A | S | G | Y | T | F | S | A | Y | W | I | E |
| | TGG | GTG | CGC | CAG | GCT | CCA | GGA | AAG | GGC | CTC | GAG | TGG | GTC | GGA | GAG | ATT | TTA | CCT |
| | W | V | R | Q | A | P | G | K | G | L | E | W | V | G | E | I | L | P |
| | GGA | AGT | AAT | AAT | TCT | AGA | TAC | AAT | GAG | AAG | TTC | AAG | GGC | CGA | GTG | ACA | GTC | ACT |
| | G | S | N | N | S | R | Y | N | E | K | F | K | G | R | V | T | V | T |
| | AGA | GAC | ACA | TCC | ACA | AAC | ACA | GCC | TAC | ATG | GAG | CTC | AGC | AGC | CTG | AGG | TCT | GAG |
| | R | D | T | S | T | N | T | A | Y | M | E | L | S | S | L | R | S | E |
| | GAC | ACA | GCC | GTC | TAT | TAC | TGT | GCA | AGA | TCC | TAC | GAC | TTT | GCC | TGG | TTT | GCT | TAC |
| | D | T | A | V | Y | Y | C | A | R | S | Y | D | F | A | W | F | A | Y |
| | TGG | GGC | CAA | GGG | ACT | CTG | GTC | ACA | GTC | TCC | TCA | GCC | TCC | ACC | AAG | GGC | CCA | TCG |
| | W | G | Q | G | T | L | V | T | V | S | S | A | S | T | K | G | P | S |
| | GTC | TTC | CCC | CTG | GCA | CCC | TCC | TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG |
| | V | F | P | L | A | P | S | S | K | S | T | S | G | G | T | A | A | L |
| | GGC | TGC | CTG | GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA |
| | G | C | L | V | K | D | Y | F | P | E | P | V | T | V | S | W | N | S |
| | GGC | GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA |
| | G | A | L | T | S | G | V | H | T | F | P | A | V | L | Q | S | S | G |

| | | | | | |
|-----------------|-----------------|-----------------|-----------------|-------------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC | AGC AGC GTG GTG | ACC GTG CCC | TCC AGC AGC TTG | GGC ACC CAG | |
| L Y S L | S S V V | T V P S | S S S L | G T Q | |
| ----- | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC | AAC GTG AAT CAC | AAG CCC AGC AAC | ACC AAG GTG GAC | AAG AAA | |
| T Y I C | N V N H | K P S N | T K V D | K K | |
| ----- | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA | TCT TGT GAC AAA | ACT CAC ACA TGC | TGT GTG GAG TGC | CCA CCG | |
| V E P K | S C D K | T H T C | C V E C | P P | |
| ----- | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| TGC CCA GCA CCT | GAA GGC GGG CTG | AAG ATC GCA GCC | TTC AAC ATC CAG | ACA TTT | |
| C P A P | E G G L | K I A A | F N I Q | T F | |
| ----- | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| GGG GAG ACC AAG | ATG TCC AAT GCC | ACC CTC GTC AGC | TAC ATT GTG CAG | ATC CTG | |
| G E T K | M S N A | T L V S | Y I V Q | I L | |
| ----- | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| AGC CGC TAC GAC | ATC GCC CTG GTC | CAG GAG GTC AGA | GAC AGC CAC CTG | ACT GCC | |
| S R Y D | I A L V | Q E V R | D S H L | T A | |
| ----- | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| GTG GGG AAG CTG | CTG GAC AAC CTC | AAT CAG GAC GCA | CCA GAC ACC TAT | CAC TAC | |
| V G K L | L D N L | N Q D A | P D T Y | H Y | |
| ----- | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| GTG GTC AGT GAG | CCA CTG GGA CGG | AAC AGC TAT AAG | GAG CGC TAC CTG | TTC GTG | |
| V V S E | P L G R | N S Y K | E R Y L | F V | |
| ----- | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| TAC AGG CCT GAC | CAG GTG TCT GCG | GTG GAC AGC TAC | TAC TAC TAC GAT | GAT GGC TGC | |
| Y R P D | Q V S A | V D S Y | Y Y Y D | D G C | |
| ----- | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| GAG CCC TGC GGG | AAC GAC ACC TTC | AAC CGA GAG CCA | GCC ATT GTC AGG | TTC TTC | |
| E P C G | N D T F | N R E P | A I V R | F F | |
| ----- | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| TCC CGG TTC ACA | GAG GTC AGG GAG | TTT GCC ATT GTT | CCC CTG CAT GCG | GCC CCG | |
| S R F T | E V R E | F A I V | P L H A | A P | |
| ----- | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|---|
| GGG | GAC | GCA | GTA | GAG | ATC | GAC | GCT | CTC | TAT | GAC | GTC | CTG | GAT | GTC | CAA | | |
| G | D | A | V | A | E | I | D | A | L | Y | D | V | Y | L | D | V | Q |

| | | | | | |
|---------------------|---------------------|---------------------|-------------|------|------|
| 1251 | 1260 | 1269 | 1278 | 1287 | 1296 |
| GAG AAA TGG GGC TTG | GAG GAC GTC ATG TTG | ATG GGC GAC TTC AAT | GCG GGC TGC | | |
| E K W G L | E D V M L M | G D F N | A G C | | |

| | | | | | |
|-------------------------|-----------------|-----------------|-------------|------|------|
| 1305 | 1314 | 1323 | 1332 | 1341 | 1350 |
| AGC TAT GTG AGA CCC TCC | CAG TGG TCA TCC | ATC CGC CTG TGG | ACA AGC CCC | ACC | |
| S Y V R P | S Q W S S | I R L W | T S P | T | |

| | | | | | |
|-------------------------|---------------------|-----------------|-------------|------|------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| TTC CAG TGG CTG ATC CCC | GAC AGC GCT GAC ACC | ACA GCT ACA CCC | ACG CAC TGT | | |
| F Q W L I P | D S A D T T | A T P T | H C | | |

| | | | | | |
|-------------------------|---------------------|-----------------|-------------|------|------|
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| GCC TAT GAC AGG ATC GTG | GTT GCA GGG ATG CTG | CTC CGA GGG GCC | GTT GTT CCC | | |
| A Y D R I V V | A G M L L | R G A V | V P | | |

| | | | | | |
|-------------------------|---------------------|-----------------|-------------|------|------|
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| GAC TCG GCT CTT CCC TTT | AAC TTC CAG GCT GCC | TAT GGC CTG AGT | GAC CAA CTG | | |
| D S A L P F N F | Q A A Y G L S | D Q L | | | |

| | | | | |
|-------------------------|---------------------|-----------------|--------|------|
| 1521 | 1530 | 1539 | 1548 | 1557 |
| GCC CAA GCC ATC AGT GAC | CAC TAT CCA GTG GAG | GTG ATG CTG AAG | TGA 3' | |
| A Q A I S D H Y | P V E V M L K | * | | |

FIGURE

(A) pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)
 Position 924 G to A by ggg to gag
 Linker GR instead of GG (position 777)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 346 a 468 c 434 g 312 t
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
  
```

//

LOCUS FDDNASE104 1560 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1560)
 /note="1 to 1560 of PAS104.dna [Split]"
 frag 721..792
 /note="1 to 72 of 104linker"
 frag join(721..>774,<776..792)
 /note="1 to 72 of 103linker [Split]"
 frag join(721..>771,<772..>774,<776..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 346 A 467 C 434 G 313 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGTC GTGGAAGTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
 901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

File : PAS104.DNA
Range : 1 1560 Mode : Normal
Codon Table : Universal

FIGURE 16(C)

| | | | | | |
|---|-----|-----|-----|-----|-----|
| 9 | 18 | 27 | 36 | 45 | 54 |
| ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC | | | | | |
| M G W S C I I L F L V A T A T G V H | | | | | |
| 63 | 72 | 81 | 90 | 99 | 108 |
| TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA | | | | | |
| S Q V Q L V Q S G A E V K K P G A S | | | | | |
| 117 | 126 | 135 | 144 | 153 | 162 |
| GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG | | | | | |
| V K V S C K A S G Y T F S A Y W I E | | | | | |
| 171 | 180 | 189 | 198 | 207 | 216 |
| TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT | | | | | |
| W V R Q A P G K G L E W V G E I L P | | | | | |
| 225 | 234 | 243 | 252 | 261 | 270 |
| GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT | | | | | |
| G S N N S R Y N E K F K G R V T V T | | | | | |
| 279 | 288 | 297 | 306 | 315 | 324 |
| AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG | | | | | |
| R D T S T N T A Y M E L S S L R S E | | | | | |
| 333 | 342 | 351 | 360 | 369 | 378 |
| GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC | | | | | |
| D T A V Y Y C A R S Y D F A W F A Y | | | | | |
| 387 | 396 | 405 | 414 | 423 | 432 |
| TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG | | | | | |
| W G Q G T L V T V S S A S T K G P S | | | | | |
| 441 | 450 | 459 | 468 | 477 | 486 |
| GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG | | | | | |
| V F P L A P S S K S T S G G T A A L | | | | | |
| 495 | 504 | 513 | 522 | 531 | 540 |
| GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA | | | | | |
| G C L V K D Y F P E P V T V S W N S | | | | | |
| 549 | 558 | 567 | 576 | 585 | 594 |
| GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA | | | | | |
| G A L T S G V H T F P A V L Q S S G | | | | | |

| | | | | | |
|---|-------------------------|-----------------------------|------|------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC AGC | AGC GTG GTG ACC GTG CCC | TCC AGC AGC TTG GGC ACC CAG | | | |
| L Y S L S S V V T V P S S S L G T Q | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA | | | | | |
| T Y I C N V N H K P S N T K V D K K | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG | | | | | |
| V E P K S C D K T H T C C V E C P P | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT | | | | | |
| C P A P E G R L K I A A F N I Q T F | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG | | | | | |
| G E T K M S N A T L V S Y I V Q I L | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC | | | | | |
| S R Y D I A L V Q E V R D S H L T A | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| GTG GAG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC | | | | | |
| V E K L L D N L N Q D A P D T Y H Y | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG | | | | | |
| V V S E P L G R N S Y K E R Y L F V | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC | | | | | |
| Y R P D Q V S A V D S Y Y Y D D G C | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC | | | | | |
| E P C G N D T F N R E P A I V R F F | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG | | | | | |
| S R F T E V R E F A I V P L H A A P | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

| | | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|--|
| GGG | GAC | GCA | GTA | GCC | GAG | ATC | GAC | GCT | CTC | TAT | GAC | GTC | TAC | CTG | GAT | GTC | CAA | |
| ----- | | | | | | | | | | | | | | | | | | |
| G | D | A | V | A | E | I | D | A | L | Y | D | V | Y | L | D | V | Q | |
| ----- | | | | | | | | | | | | | | | | | | |
| 1251 | | | | 1260 | | | 1269 | | | 1278 | | | 1287 | | | 1296 | | |
| GAG | AAA | TGG | GGC | TTG | GAG | GAC | GTC | ATG | TTG | ATG | GGC | GAC | TTC | AAT | GCG | GGC | TGC | |
| ----- | | | | | | | | | | | | | | | | | | |
| E | K | W | G | L | E | D | V | M | L | M | G | D | F | N | A | G | C | |
| ----- | | | | | | | | | | | | | | | | | | |
| 1305 | | | | 1314 | | | 1323 | | | 1332 | | | 1341 | | | 1350 | | |
| AGC | TAT | GTG | AGA | CCC | TCC | CAG | TGG | TCA | TCC | ATC | CGC | CTG | TGG | ACA | AGC | CCC | ACC | |
| ----- | | | | | | | | | | | | | | | | | | |
| S | Y | V | R | P | S | Q | W | S | S | I | R | L | W | T | S | P | T | |
| ----- | | | | | | | | | | | | | | | | | | |
| 1359 | | | | 1368 | | | 1377 | | | 1386 | | | 1395 | | | 1404 | | |
| TTC | CAG | TGG | CTG | ATC | CCC | GAC | AGC | GCT | GAC | ACC | ACA | GCT | ACA | CCC | ACG | CAC | TGT | |
| ----- | | | | | | | | | | | | | | | | | | |
| F | Q | W | L | I | P | D | S | A | D | T | T | A | T | P | T | H | C | |
| ----- | | | | | | | | | | | | | | | | | | |
| 1413 | | | | 1422 | | | 1431 | | | 1440 | | | 1449 | | | 1458 | | |
| GCC | TAT | GAC | AGG | ATC | GTG | GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT | GTT | CCC | |
| ----- | | | | | | | | | | | | | | | | | | |
| A | Y | D | R | I | V | V | A | G | M | L | L | R | G | A | V | V | P | |
| ----- | | | | | | | | | | | | | | | | | | |
| 1467 | | | | 1476 | | | 1485 | | | 1494 | | | 1503 | | | 1512 | | |
| GAC | TCG | GCT | CTT | CCC | TTT | AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC | CAA | CTG | |
| ----- | | | | | | | | | | | | | | | | | | |
| D | S | A | L | P | F | N | F | Q | A | A | Y | G | L | S | D | Q | L | |
| ----- | | | | | | | | | | | | | | | | | | |
| 1521 | | | | 1530 | | | 1539 | | | 1548 | | | 1557 | | | | | |
| GCC | CAA | GCC | ATC | AGT | GAC | CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | TGA | 3' | | |
| ----- | | | | | | | | | | | | | | | | | | |
| A | Q | A | I | S | D | H | Y | P | V | E | V | M | L | K | * | | | |

(A) pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS105)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 353 a 473 c 442 g 310 t
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTTGA

```

//

L NLS

Figure 17(B)

LOCUS FDDNASE105 1578 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES

Location/Qualifiers
 frag join(1..>720,<781..1578)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 721..780
 /note="1 to 60 of 101/105linker"
 frag join(721..>735,<736..>759,<760..>780)
 /note="1 to 80 of 102linker [Split]"

BASE COUNT 353 A 471 C 443 G 311 T 0 OTHER
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 121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCGGGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
 1561 AAGAAGCGCA AGGTTTGA

Figure 1(k)

LOCUS FDDNASE105 1587 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
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 frag join(10..>729,<790..1587)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"

BASE COUNT 354 A 477 C 445 G 311 T 0 OTHER

ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACCTAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGAATCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAACCTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
 781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
 841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
 961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
 1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
 1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTT
 1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCAGGGGA CGCAGTAGCC
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
 1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
 1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
 1381 ACAGCTACAC CCACGCACTG TGCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
 1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTAACTTCC AGGCTGCCTA TGGCCTGAGT
 1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC
 1561 GGACCCAAAA AGAAGCGCAA GGTTTGA

File : PAS105.DN
Range : 1 1578 Mode : Normal
Codon Table : Universal

FIGURE 17 (D)

| | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5' | ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TTC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | GTC | CAC |
| | M | G | W | S | C | I | I | L | F | L | V | A | T | A | T | G | V | H |
| | | | | | | | | | | | | | | | | | | |
| | TCC | CAG | GTG | CAG | CTG | GTG | CAG | TCT | GGG | GCA | GAG | GTG | AAA | AAG | CCT | GGG | GCC | TCA |
| | S | Q | V | Q | L | V | Q | S | G | A | E | V | K | K | P | G | A | S |
| | | | | | | | | | | | | | | | | | | |
| | GTG | AAG | GTG | TCC | TGC | AAG | GCT | TCT | GGC | TAC | ACC | TTC | AGT | GCC | TAC | TGG | ATA | GAG |
| | V | K | V | S | C | K | A | S | G | Y | T | F | S | A | Y | W | I | E |
| | | | | | | | | | | | | | | | | | | |
| | TGG | GTG | CGC | CAG | GCT | CCA | GGA | AAG | GGC | CTC | GAG | TGG | GTC | GGA | GAG | ATT | TTA | CCT |
| | W | V | R | Q | A | P | G | K | G | L | E | W | V | G | E | I | L | P |
| | | | | | | | | | | | | | | | | | | |
| | GGA | AGT | AAT | AAT | TCT | AGA | TAC | AAT | GAG | AAG | TTC | AAG | GGC | CGA | GTG | ACA | GTC | ACT |
| | G | S | N | N | S | R | Y | N | E | K | F | K | G | R | V | T | V | T |
| | | | | | | | | | | | | | | | | | | |
| | AGA | GAC | ACA | TCC | ACA | AAC | ACA | GCC | TAC | ATG | GAG | CTC | AGC | AGC | CTG | AGG | TCT | GAG |
| | R | D | T | S | T | N | T | A | Y | M | E | L | S | S | L | R | S | E |
| | | | | | | | | | | | | | | | | | | |
| | GAC | ACA | GCC | GTC | TAT | TAC | TGT | GCA | AGA | TCC | TAC | GAC | TTT | GCC | TGG | TTT | GCT | TAC |
| | D | T | A | V | Y | Y | C | A | R | S | Y | D | F | A | W | F | A | Y |
| | | | | | | | | | | | | | | | | | | |
| | TGG | GGC | CAA | GGG | ACT | CTG | GTC | ACA | GTC | TCC | TCA | GCC | TCC | ACC | AAG | GGC | CCA | TCG |
| | W | G | Q | G | T | L | V | T | V | S | S | A | S | T | K | G | P | S |
| | | | | | | | | | | | | | | | | | | |
| | GTC | TTC | CCC | CTG | GCA | CCC | TCC | TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG |
| | V | F | P | L | A | P | S | S | K | S | T | S | G | G | T | A | A | L |
| | | | | | | | | | | | | | | | | | | |
| | GGC | TGC | CTG | GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA |
| | G | C | L | V | K | D | Y | F | P | E | P | V | T | V | S | W | N | S |
| | | | | | | | | | | | | | | | | | | |
| | GGC | GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA |
| | G | A | L | T | S | G | V | H | T | F | P | A | V | L | Q | S | S | G |

- 1 -

| | | | | | |
|---|------|------|------|------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG | | | | | |
| L Y S L S S V V T V P S S S L G T Q | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA | | | | | |
| T Y I C N V N H K P S N T K V D K K | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT | | | | | |
| V E P K S C D K T H T C P P C P A P | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG | | | | | |
| E G G L K I A A F N I Q T F G E T K | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC | | | | | |
| M S N A T L V S Y I V Q I L S R Y D | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG | | | | | |
| I A L V Q E V R D S H L T A V G K L | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG | | | | | |
| L D N L N Q D A P D T Y H Y V V S E | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC | | | | | |
| P L G R N S Y K E R Y L F V Y R P D | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG | | | | | |
| Q V S A V D S Y Y Y D D G C E P C G | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA | | | | | |
| N D T F N R E P A I V R F F S R F T | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA | | | | | |
| E V R E F A I V P L H A A P G D A V | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

GCC GAG ATC GAT TCT CTC TAT GAC GTC TAC CTG GAT GTC GAG AAA TGG GGC

 A E I D A L Y D V Y L D V Q E K W G

1251 1260 1269 1278 1287 1296
 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA

 L E D V M L M G D F N A G C S Y V R

1305 1314 1323 1332 1341 1350
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 P S Q W S S I R L W T S P T F Q W L

1359 1368 1377 1386 1395 1404
 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG

 I P D S A D T T A T P T H C A Y D R

1413 1422 1431 1440 1449 1458
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 I V V A G M L L R G A V V P D S A L

1467 1476 1485 1494 1503 1512
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 P F N F Q A A Y G L S D Q L A Q A I

1521 1530 1539 1548 1557 1566
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG

 S D H Y P V E V M L K G G G P K K K

1575
 CGC AAG GTT TGA 3'

 R K V *

FIGURE 1

(A) pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS106)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 355 a 475 c 452 g 314 t
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
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181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
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661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
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841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
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1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAAGTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

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↳ NLS

LOCUS FDDNASE106 1596 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
 frag join(1..>720,<799..1596)
 /note="1 to 1596 of PAS106.dna [Split]"
 frag 721..798
 /note="1 to 78 of 102/106linker"

BASE COUNT 355 A 474 C 452 G 315 T 0 OTHER

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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACCTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
 1021 TACCTGTTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAGC CAGCCATTGT CAGGTTCTTC
 1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
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LOCUS FDDNASE106 1605 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag 10..1605

/note="1 to 1596 of FdDNase106correct"

frag join(10..>729,<808..1605)

/note="1 to 1596 of PAS106.dna [Split]"

frag 730..807

/note="1 to 78 of 102/106linker"

BASE COUNT 356 A 480 C 454 G 315 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG

121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC

181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT

241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTACTA GAGACACATC CACAAACACA

301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA

361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA

421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG

481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG

541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA

601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC

661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC

721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG

781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG

841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG

901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT

961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT

1021 AAGGAGCGCT ACCTGTTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC

1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC

1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC

1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG

1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG

1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC

1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT

1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG

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File : PAS106.DNA
Range : 1 - 596 Mode : Normal
Codon Table : Universal

FIGURE 18(D)

| | | | | | |
|---|-----|-----|-----|-----|-----|
| 9 | 18 | 27 | 36 | 45 | 54 |
| ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC | | | | | |
| M G W S C I I L F L V A T A T G V H | | | | | |
| 63 | 72 | 81 | 90 | 99 | 108 |
| TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA | | | | | |
| S Q V Q L V Q S G A E V K K P G A S | | | | | |
| 117 | 126 | 135 | 144 | 153 | 162 |
| GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG | | | | | |
| V K V S C K A S G Y T F S A Y W I E | | | | | |
| 171 | 180 | 189 | 198 | 207 | 216 |
| TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT | | | | | |
| W V R Q A P G K G L E W V G E I L P | | | | | |
| 225 | 234 | 243 | 252 | 261 | 270 |
| GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT | | | | | |
| G S N N S R Y N E K F K G R V T V T | | | | | |
| 279 | 288 | 297 | 306 | 315 | 324 |
| AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG | | | | | |
| R D T S T N T A Y M E L S S L R S E | | | | | |
| 333 | 342 | 351 | 360 | 369 | 378 |
| GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC | | | | | |
| D T A V Y Y C A R S Y D F A W F A Y | | | | | |
| 387 | 396 | 405 | 414 | 423 | 432 |
| TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG | | | | | |
| W G Q G T L V T V S S A S T K G P S | | | | | |
| 441 | 450 | 459 | 468 | 477 | 486 |
| GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG | | | | | |
| V F P L A P S S K S T S G G T A A L | | | | | |
| 495 | 504 | 513 | 522 | 531 | 540 |
| GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA | | | | | |
| G C L V K D Y F P E P V T V S W N S | | | | | |
| 549 | 558 | 567 | 576 | 585 | 594 |
| GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA | | | | | |
| G A L T S G V H T F P A V L Q S S G | | | | | |

| | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|------|-----|-----|-----|------|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|------|-----|-----|-----|------|-----|
| CTC | TAC | 603 | CTC | AGC | 612 | AGC | GTG | GTG | 621 | ACC | GTG | CCC | TCC | AGC | 630 | AGC | AGC | 639 | TTG | GGC | ACC | 648 | CAG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| L | Y | S | L | S | S | V | V | T | V | P | S | S | S | S | L | G | T | Q | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| ACC | TAC | 657 | ATC | TGC | AAC | 666 | GTG | AAT | CAC | 675 | AAG | CCC | AGC | AAC | 684 | ACC | AAG | 693 | GTG | GAC | AAG | 702 | AAA |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| T | Y | I | C | N | V | N | H | K | P | S | N | T | K | V | D | K | K | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| GTT | GAG | 711 | CCC | AAA | TCT | 720 | TGT | GAC | AAA | 729 | ACT | CAC | ACA | TGC | 738 | TGT | GTG | 747 | GAG | TGC | CCA | 756 | CCG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| V | E | P | K | S | C | D | K | T | H | T | C | C | V | E | C | P | P | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| TGC | CCA | 765 | GCA | CCT | GAA | 774 | GGG | AGC | GGC | 783 | GGG | CTG | AAG | ATC | 792 | GCA | GCC | 801 | TTC | AAC | ATC | 810 | CAG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| C | P | A | P | E | G | S | G | G | L | K | I | A | A | F | N | I | Q | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| ACA | TTT | 819 | GGG | GAG | ACC | 828 | AAG | ATG | TCC | 837 | AAT | GCC | ACC | CTC | 846 | GTC | AGC | 855 | TAC | ATT | GTG | 864 | CAG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| T | F | G | E | T | K | M | S | N | A | T | L | V | S | Y | I | V | Q | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| ATC | CTG | 873 | AGC | CGC | TAC | 882 | GAC | ATC | GCC | 891 | CTG | GTC | CAG | GAG | 900 | GTC | AGA | 909 | GAC | AGC | CAC | 918 | CTG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| I | L | S | R | Y | D | I | A | L | V | Q | E | V | R | D | S | H | L | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| ACT | GCC | 927 | GTG | GGG | AAG | 936 | CTG | CTG | GAC | 945 | AAC | CTC | AAT | CAG | 954 | GAC | GCA | 963 | CCA | GAC | ACC | 972 | TAT |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| T | A | V | G | K | L | L | D | N | L | N | Q | D | A | P | D | T | Y | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| CAC | TAC | 981 | GTG | GTC | AGT | 990 | GAG | CCA | CTG | 999 | GGA | CGG | AAC | AGC | 1008 | TAT | AAG | 1017 | GAG | CGC | TAC | 1026 | CTG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| H | Y | V | V | S | E | P | L | G | R | N | S | Y | K | E | R | Y | L | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| TTC | GTG | 1035 | TAC | AGG | CCT | 1044 | GAC | CAG | GTG | 1053 | TCT | GCG | GTG | GAC | 1062 | AGC | TAC | 1071 | TAC | TAC | GAT | 1080 | GAT |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| F | V | Y | R | P | D | Q | V | S | A | V | D | S | Y | Y | Y | D | D | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| GGC | TGC | 1089 | GAG | CCC | TGC | 1098 | GGG | AAC | GAC | 1107 | ACC | TTC | AAC | CGA | 1116 | GAG | CCA | 1125 | GCC | ATT | GTC | 1134 | AGG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| G | C | E | P | C | G | N | D | T | F | N | R | E | P | A | I | V | R | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| TTC | TTC | 1143 | TCC | CGG | TTC | 1152 | ACA | GAG | GTC | 1161 | AGG | GAG | TTT | GCC | 1170 | ATT | GTT | 1179 | CCC | CTG | CAT | 1188 | GCG |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| F | F | S | R | F | T | E | V | R | E | F | A | I | V | P | L | H | A | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | |
| | | 1197 | | | | 1206 | | | | 1215 | | | | | 1224 | | | 1233 | | | | 1242 | |

| | | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|--|
| GCC | CCG | GGG | GAC | CAA | GTA | GCC | GAG | ATC | GAC | GCT | CTC | TAT | CAA | GTC | TAC | CTG | GAT | |
| ----- | | | | | | | | | | | | | | | | | | |
| A | P | G | D | A | V | A | E | I | D | A | L | Y | D | V | Y | L | D | |
| | | | | | | | | | | | | | | | | | | |
| 1251 | | | | 1260 | | | 1269 | | | 1278 | | | 1287 | | | 1296 | | |
| GTC | CAA | GAG | AAA | TGG | GGC | TTG | GAG | GAC | GTC | ATG | TTG | ATG | GGC | GAC | TTC | AAT | GCG | |
| ----- | | | | | | | | | | | | | | | | | | |
| V | Q | E | K | W | G | L | E | D | V | M | L | M | G | D | F | N | A | |
| | | | | | | | | | | | | | | | | | | |
| 1305 | | | | 1314 | | | 1323 | | | 1332 | | | 1341 | | | 1350 | | |
| GGC | TGC | AGC | TAT | GTG | AGA | CCC | TCC | CAG | TGG | TCA | TCC | ATC | CGC | CTG | TGG | ACA | AGC | |
| ----- | | | | | | | | | | | | | | | | | | |
| G | C | S | Y | V | R | P | S | Q | W | S | S | I | R | L | W | T | S | |
| | | | | | | | | | | | | | | | | | | |
| 1359 | | | | 1368 | | | 1377 | | | 1386 | | | 1395 | | | 1404 | | |
| CCC | ACC | TTC | CAG | TGG | CTG | ATC | CCC | GAC | AGC | GCT | GAC | ACC | ACA | GCT | ACA | CCC | ACG | |
| ----- | | | | | | | | | | | | | | | | | | |
| P | T | F | Q | W | L | I | P | D | S | A | D | T | T | A | T | P | T | |
| | | | | | | | | | | | | | | | | | | |
| 1413 | | | | 1422 | | | 1431 | | | 1440 | | | 1449 | | | 1458 | | |
| CAC | TGT | GCC | TAT | GAC | AGG | ATC | GTG | GTT | GCA | GGG | ATG | CTG | CTC | CGA | GGG | GCC | GTT | |
| ----- | | | | | | | | | | | | | | | | | | |
| H | C | A | Y | D | R | I | V | V | A | G | M | L | L | R | G | A | V | |
| | | | | | | | | | | | | | | | | | | |
| 1467 | | | | 1476 | | | 1485 | | | 1494 | | | 1503 | | | 1512 | | |
| GTT | CCC | GAC | TCG | GCT | CTT | CCC | TTT | AAC | TTC | CAG | GCT | GCC | TAT | GGC | CTG | AGT | GAC | |
| ----- | | | | | | | | | | | | | | | | | | |
| V | P | D | S | A | L | P | F | N | F | Q | A | A | Y | G | L | S | D | |
| | | | | | | | | | | | | | | | | | | |
| 1521 | | | | 1530 | | | 1539 | | | 1548 | | | 1557 | | | 1566 | | |
| CAA | CTG | GCC | CAA | GCC | ATC | AGT | GAC | CAC | TAT | CCA | GTG | GAG | GTG | ATG | CTG | AAG | GGG | |
| ----- | | | | | | | | | | | | | | | | | | |
| Q | L | A | Q | A | I | S | D | H | Y | P | V | E | V | M | L | K | G | |
| | | | | | | | | | | | | | | | | | | |
| 1575 | | | | 1584 | | | 1593 | | | | | | | | | | | |
| GGC | GGA | CCC | AAA | AAG | AAG | CGC | AAG | GTT | TGA | 3' | | | | | | | | |
| ----- | | | | | | | | | | | | | | | | | | |
| G | G | P | K | K | K | R | K | V | * | | | | | | | | | |

(A) pAS107

LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS107)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 354 a 474 c 448 g 314 t
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
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181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
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↳ NLS

LOCUS FDDNASE107 1590 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag join(1..>720,<793..1590)

frag 721..792

frag join(721..>771,<772..792)

BASE COUNT 354 A 473 C 448 G 315 T 0 OTHER

ORIGIN -

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| 61 | GTGCAGCTGG | TGCAGTCTGG | GGCAGAGGTG | AAAAAGCCTG | GGGCCTCAGT | GAAGGTGTCC |
| 121 | TGCAAGGCTT | CTGGCTACAC | CTTCAGTGCC | TACTGGATAG | AGTGGGTGCG | CCAGGCTCCA |
| 181 | GGAAAGGGCC | TCGAGTGGGT | CGGAGAGATT | TTACCTGGAA | GTAATAATTC | TAGATACAAT |
| 241 | GAGAAGTTCA | AGGGCCGAGT | GACAGTCACT | AGAGACACAT | CCACAAACAC | AGCCTACATG |
| 301 | GAGCTCAGCA | GCCTGAGGTC | TGAGGACACA | GCCGTCTATT | ACTGTGCAAG | ATCCTACGAC |
| 361 | TTTGCCTGGT | TTGCTTACTG | GGGCCAAGGG | ACTCTGGTCA | CAGTCTCCTC | AGCCTCCACC |
| 421 | AAGGGCCCAT | CGGTCTTCCC | CCTGGCACCC | TCCTCCAAGA | GCACCTCTGG | GGGCACAGCG |
| 481 | GCCCTGGGCT | GCCTGGTCAA | GGACTACTTC | CCCGAACCGG | TGACGGTGTC | GTGGAACTCA |
| 541 | GGCGCCCTGA | CCAGCGGCGT | GCACACCTTC | CCGGCTGTCC | TACAGTCCTC | AGGACTCTAC |
| 601 | TCCCTCAGCA | GCGTGGTGAC | CGTGCCCTCC | AGCAGCTTGG | GCACCCAGAC | CTACATCTGC |
| 661 | AACGTGAATC | ACAAGCCCAG | CAACACCAAG | GTGGACAAGA | AAGTTGAGCC | CAAATCTTGT |
| 721 | GACAAAACCTC | ACACATGCTG | TGTCGAGTGT | CCACCGTGTC | CAGCACCAGA | GGGCGGGCTG |
| 781 | AAGATCGCAG | CCTTCAACAT | CCAGACATTT | GGGGAGACCA | AGATGTCCAA | TGCCACCCTC |
| 841 | GTCAGCTACA | TTGTGCAGAT | CCTGAGCCGC | TACGACATCG | CCCTGGTCCA | GGAGGTCAGA |
| 901 | GACAGCCACC | TGACTGCCGT | GGGGAAGCTG | CTGGACAACC | TCAATCAGGA | CGCACCAGAC |
| 961 | ACCTATCACT | ACGTGGTCAG | TGAGCCACTG | GGACGGAACA | GCTATAAGGA | GCGCTACCTG |
| 1021 | TTCGTGTACA | GGCCTGACCA | GGTGTCTGCG | GTGGACAGCT | ACTACTACGA | TGATGGCTGC |
| 1081 | GAGCCCTGCG | GGAACGACAC | CTTCAACCGA | GAGCCAGCCA | TTGTCAGGTT | CTTCTCCCGG |
| 1141 | TTCACAGAGG | TCAGGGAGTT | TGCCATTGTT | CCCCTGCATG | CGGCCCCGGG | GGACGCAGTA |
| 1201 | GCCGAGATCG | ACGCTCTCTA | TGACGTCTAC | CTGGATGTCC | AAGAGAAATG | GGGCTTGGAG |
| 1261 | GACGTCATGT | TGATGGGCGA | CTTCAATGCG | GGCTGCAGCT | ATGTGAGACC | CTCCCAGTGG |
| 1321 | TCATCCATCC | GCCTGTGGAC | AAGCCCCACC | TTCCAGTGGC | TGATCCCCGA | CAGCGCTGAC |
| 1381 | ACCACAGCTA | CACCCACGCA | CTGTGCCTAT | GACAGGATCG | TGGTTGCAGG | GATGCTGCTC |
| 1441 | CGAGGGGCGG | TTGTTCCCGA | CTCGGCTCTT | CCCTTTAACT | TCCAGGCTGC | CTATGGCCTG |
| 1501 | AGTGACCAAC | TGGCCCAAGC | CATCAGTGAC | CACTATCCAG | TGGAGGTGAT | GCTGAAGGGG |
| 1561 | GGCGGACCCA | AAAAGAAGCG | CAAGGTTTGA | | | |

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 ACCESSION -
 KEYWORDS -
 SOURCE -
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 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 355 A 479 C 450 G 315 T 0 OTHER
 ORIGIN -

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61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGG
541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
1381 AGCGCTGACA CCACAGCTAC ACCCAGGCAC TGTGCCTATG ACAGGATCGT GGTGTCAGGG
1441 ATGCTGCTCC GAGGGGCCGT TGTTCGCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA

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FIGURE 19 (0)

| | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5' | ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TTC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | GTC | CAC |
| | M | G | W | S | C | I | I | L | F | L | V | A | T | A | T | G | V | H |
| | | | | | | | | | | | | | | | | | | |
| | TCC | CAG | GTG | CAG | CTG | GTG | CAG | TCT | GGG | GCA | GAG | GTG | AAA | AAG | CCT | GGG | GCC | TCA |
| | S | Q | V | Q | L | V | Q | S | G | A | E | V | K | K | P | G | A | S |
| | | | | | | | | | | | | | | | | | | |
| | GTG | AAG | GTG | TCC | TGC | AAG | GCT | TCT | GGC | TAC | ACC | TTC | AGT | GCC | TAC | TGG | ATA | GAG |
| | V | K | V | S | C | K | A | S | G | Y | T | F | S | A | Y | W | I | E |
| | | | | | | | | | | | | | | | | | | |
| | TGG | GTG | CGC | CAG | GCT | CCA | GGA | AAG | GGC | CTC | GAG | TGG | GTC | GGA | GAG | ATT | TTA | CCT |
| | W | V | R | Q | A | P | G | K | G | L | E | W | V | G | E | I | L | P |
| | | | | | | | | | | | | | | | | | | |
| | GGA | AGT | AAT | AAT | TCT | AGA | TAC | AAT | GAG | AAG | TTC | AAG | GGC | CGA | GTG | ACA | GTC | ACT |
| | G | S | N | N | S | R | Y | N | E | K | F | K | G | R | V | T | V | T |
| | | | | | | | | | | | | | | | | | | |
| | AGA | GAC | ACA | TCC | ACA | AAC | ACA | GCC | TAC | ATG | GAG | CTC | AGC | AGC | CTG | AGG | TCT | GAG |
| | R | D | T | S | T | N | T | A | Y | M | E | L | S | S | L | R | S | E |
| | | | | | | | | | | | | | | | | | | |
| | GAC | ACA | GCC | GTC | TAT | TAC | TGT | GCA | AGA | TCC | TAC | GAC | TTT | GCC | TGG | TTT | GCT | TAC |
| | D | T | A | V | Y | Y | C | A | R | S | Y | D | F | A | W | F | A | Y |
| | | | | | | | | | | | | | | | | | | |
| | TGG | GGC | CAA | GGG | ACT | CTG | GTC | ACA | GTC | TCC | TCA | GCC | TCC | ACC | AAG | GGC | CCA | TCG |
| | W | G | Q | G | T | L | V | T | V | S | S | A | S | T | K | G | P | S |
| | | | | | | | | | | | | | | | | | | |
| | GTC | TTC | CCC | CTG | GCA | CCC | TCC | TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG |
| | V | F | P | L | A | P | S | S | K | S | T | S | G | G | T | A | A | L |
| | | | | | | | | | | | | | | | | | | |
| | GGC | TGC | CTG | GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA |
| | G | C | L | V | K | D | Y | F | P | E | P | V | T | V | S | W | N | S |
| | | | | | | | | | | | | | | | | | | |
| | GGC | GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA |
| | G | A | L | T | S | G | V | H | T | F | P | A | V | L | Q | S | S | G |

- 1 -

| | | | | | |
|---------------------|-------------------------|-----------------------------|-------------|------|------|
| 603 | 612 | 621 | 630 | 639 | 648 |
| CTC TAC TCC CTC AGC | AGC GTG GTG ACC GTG CCC | TCC AGC AGC TTG GGC ACC CAG | | | |
| --- | --- | --- | --- | --- | --- |
| L Y S L S | S V V T V P S S S | L G T Q | | | |
| | | | | | |
| 657 | 666 | 675 | 684 | 693 | 702 |
| ACC TAC ATC TGC AAC | GTG AAT CAC AAG CCC | AGC AAC ACC AAG GTG | GAC AAG AAA | | |
| --- | --- | --- | --- | --- | --- |
| T Y I C N | V N H K P S N T K | V D K K | | | |
| | | | | | |
| 711 | 720 | 729 | 738 | 747 | 756 |
| GTT GAG CCC AAA TCT | TGT GAC AAA ACT CAC | ACA TGC TGT GTG GAG | TGC CCA CCG | | |
| --- | --- | --- | --- | --- | --- |
| V E P K S | C D K T H T C C | V E C P P | | | |
| | | | | | |
| 765 | 774 | 783 | 792 | 801 | 810 |
| TGC CCA GCA CCT GAA | GGC GGG CTG AAG ATC | GCA GCC TTC AAC ATC | CAG ACA TTT | | |
| --- | --- | --- | --- | --- | --- |
| C P A P E | G G L K I A A F | N I Q T F | | | |
| | | | | | |
| 819 | 828 | 837 | 846 | 855 | 864 |
| GGG GAG ACC AAG ATG | TCC AAT GCC ACC CTC | GTC AGC TAC ATT GTG | CAG ATC CTG | | |
| --- | --- | --- | --- | --- | --- |
| G E T K M | S N A T L V S Y I | V Q I L | | | |
| | | | | | |
| 873 | 882 | 891 | 900 | 909 | 918 |
| AGC CGC TAC GAC ATC | GCC CTG GTC CAG GAG | GTC AGA GAC AGC CAC | CTG ACT GCC | | |
| --- | --- | --- | --- | --- | --- |
| S R Y D I | A L V Q E V R D S | H L T A | | | |
| | | | | | |
| 927 | 936 | 945 | 954 | 963 | 972 |
| GTG GGG AAG CTG CTG | GAC AAC CTC AAT CAG | GAC GCA CCA GAC ACC | TAT CAC TAC | | |
| --- | --- | --- | --- | --- | --- |
| V G K L L | D N L N Q D A P | D T Y H Y | | | |
| | | | | | |
| 981 | 990 | 999 | 1008 | 1017 | 1026 |
| GTG GTC AGT GAG CCA | CTG GGA CGG AAC AGC | TAT AAG GAG CGC TAC | CTG TTC GTG | | |
| --- | --- | --- | --- | --- | --- |
| V V S E P | L G R N S Y K E | R Y L F V | | | |
| | | | | | |
| 1035 | 1044 | 1053 | 1062 | 1071 | 1080 |
| TAC AGG CCT GAC CAG | GTG TCT GCG GTG GAC | AGC TAC TAC TAC GAT | GAT GGC TGC | | |
| --- | --- | --- | --- | --- | --- |
| Y R P D Q | V S A V D S Y Y | Y D D G C | | | |
| | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| GAG CCC TGC GGG AAC | GAC ACC TTC AAC CGA | GAG CCA GCC ATT GTC | AGG TTC TTC | | |
| --- | --- | --- | --- | --- | --- |
| E P C G N | D T F N R E P A | I V R F F | | | |
| | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| TCC CGG TTC ACA GAG | GTC AGG GAG TTT GCC | ATT GTT CCC CTG CAT | GCG GCC CCG | | |
| --- | --- | --- | --- | --- | --- |
| S R F T E | V R E F A I V P | L H A A P | | | |
| | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|---|
| GGG | GAC | GCA | GTA | GAG | ATC | GAC | GCT | CTC | TAT | GAC | GTC | CTG | GAT | GTC | CAA | | |
| G | D | A | V | A | E | I | D | A | L | Y | D | V | Y | L | D | V | Q |

| | | | | | |
|---------------------|---------------------|-----------------|-----------------|------|------|
| 1251 | 1260 | 1269 | 1278 | 1287 | 1296 |
| GAG AAA TGG GGC TTG | GAG GAC GTC ATG TTG | ATG GGC GAC TTC | AAT GCG GGC TGC | | |
| E K W G L | E D V M L M | G D F N | A G C | | |

| | | | | | |
|-------------------------|-----------------|-----------------|-----------------|------|------|
| 1305 | 1314 | 1323 | 1332 | 1341 | 1350 |
| AGC TAT GTG AGA CCC TCC | CAG TGG TCA TCC | ATC CGC CTG TGG | ACA AGC CCC ACC | | |
| S Y V R P | S Q W S S | I R L W | T S P | | |

| | | | | | |
|-------------------------|---------------------|-----------------|-------------|------|------|
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| TTC CAG TGG CTG ATC CCC | GAC AGC GCT GAC ACC | ACA GCT ACA CCC | ACG CAC TGT | | |
| F Q W L I P | D S A D T T | A T P T | H C | | |

| | | | | | |
|-------------------------|---------------------|-----------------|-------------|------|------|
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| GCC TAT GAC AGG ATC GTG | GTT GCA GGG ATG CTG | CTC CGA GGG GCC | GTT GTT CCC | | |
| A Y D R I V | V A G M L L | R G A V | V P | | |

| | | | | | |
|-------------------------|---------------------|-----------------|-------------|------|------|
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| GAC TCG GCT CTT CCC TTT | AAC TTC CAG GCT GCC | TAT GGC CTG AGT | GAC CAA CTG | | |
| D S A L P F | N F Q A A Y | G L S D | Q L | | |

| | | | | | |
|-------------------------|---------------------|-----------------|-------------|------|------|
| 1521 | 1530 | 1539 | 1548 | 1557 | 1566 |
| GCC CAA GCC ATC AGT GAC | CAC TAT CCA GTG GAG | GTG ATG CTG AAG | GGG GGC GGA | | |
| A Q A I S D | H Y P V E V | M L K G | G G | | |

| | |
|---------------------|----------------|
| 1575 | 1584 |
| CCC AAA AAG AAG CGC | AAG GTT TGA 3' |
| P K K K R K | V * |

Fig 20 Mammalian expression of humanised HMFG1-DNase constructs

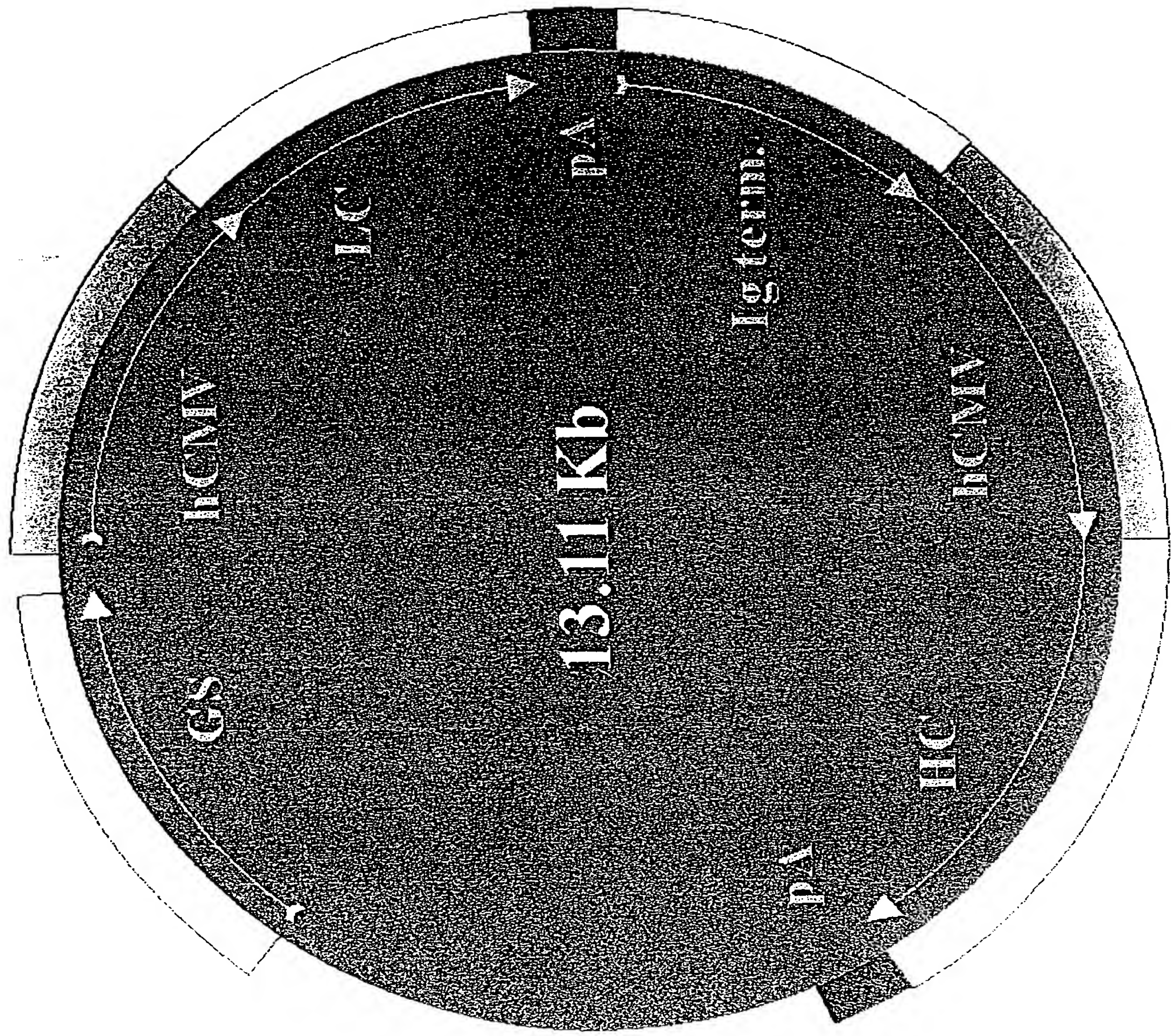
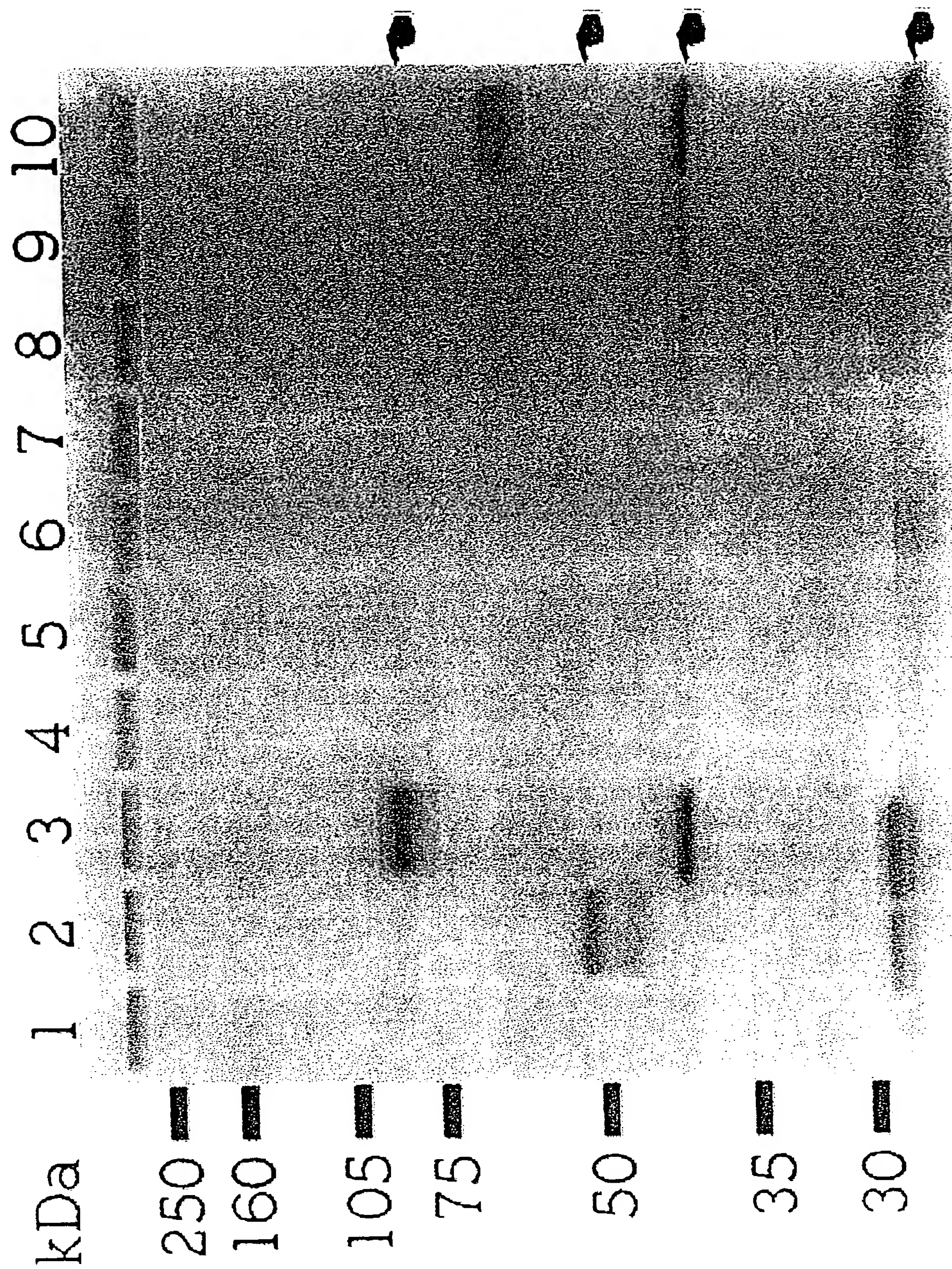
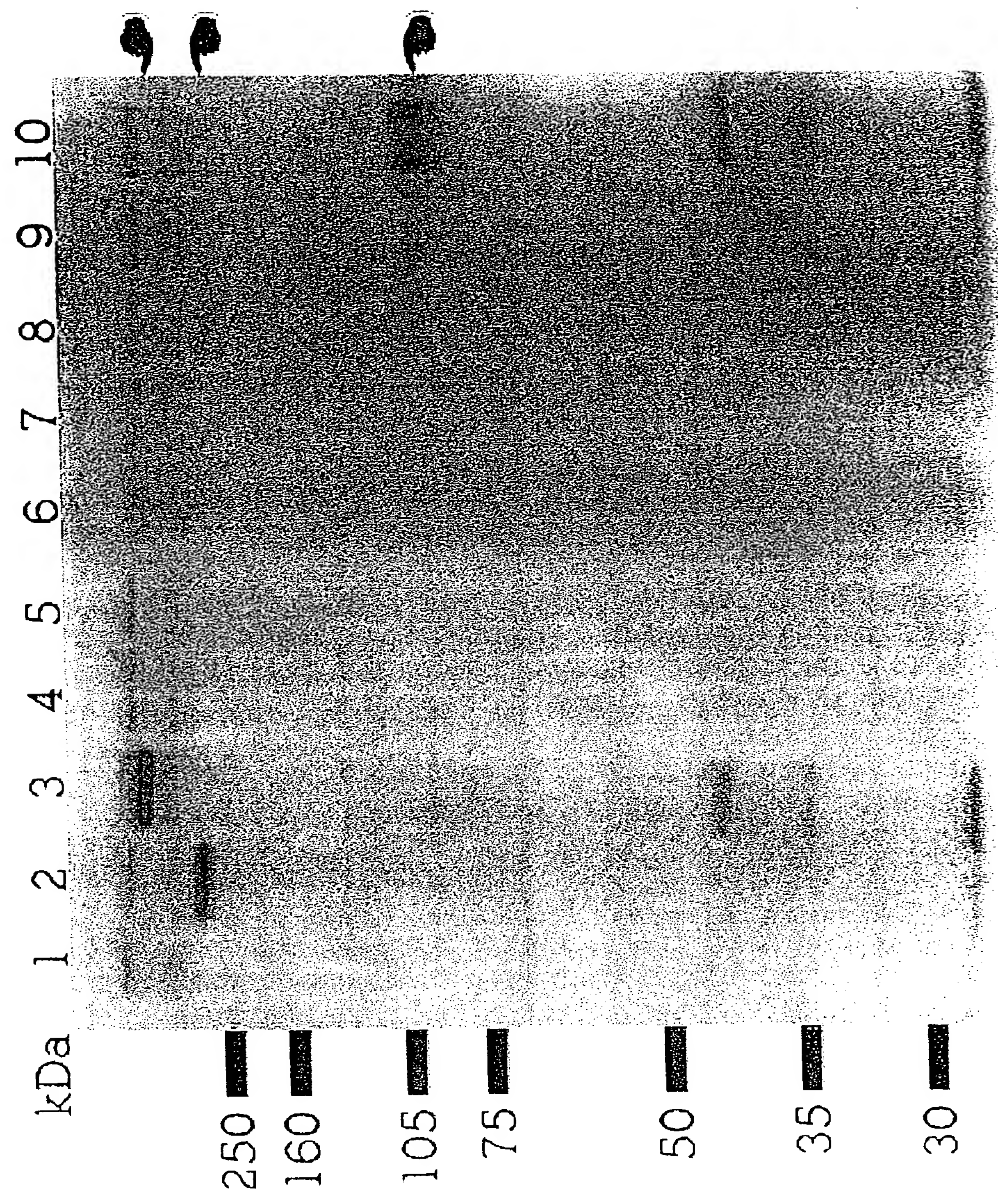


Fig 21(A) Immuno-precipitation of metabolically labelled transient transfectants



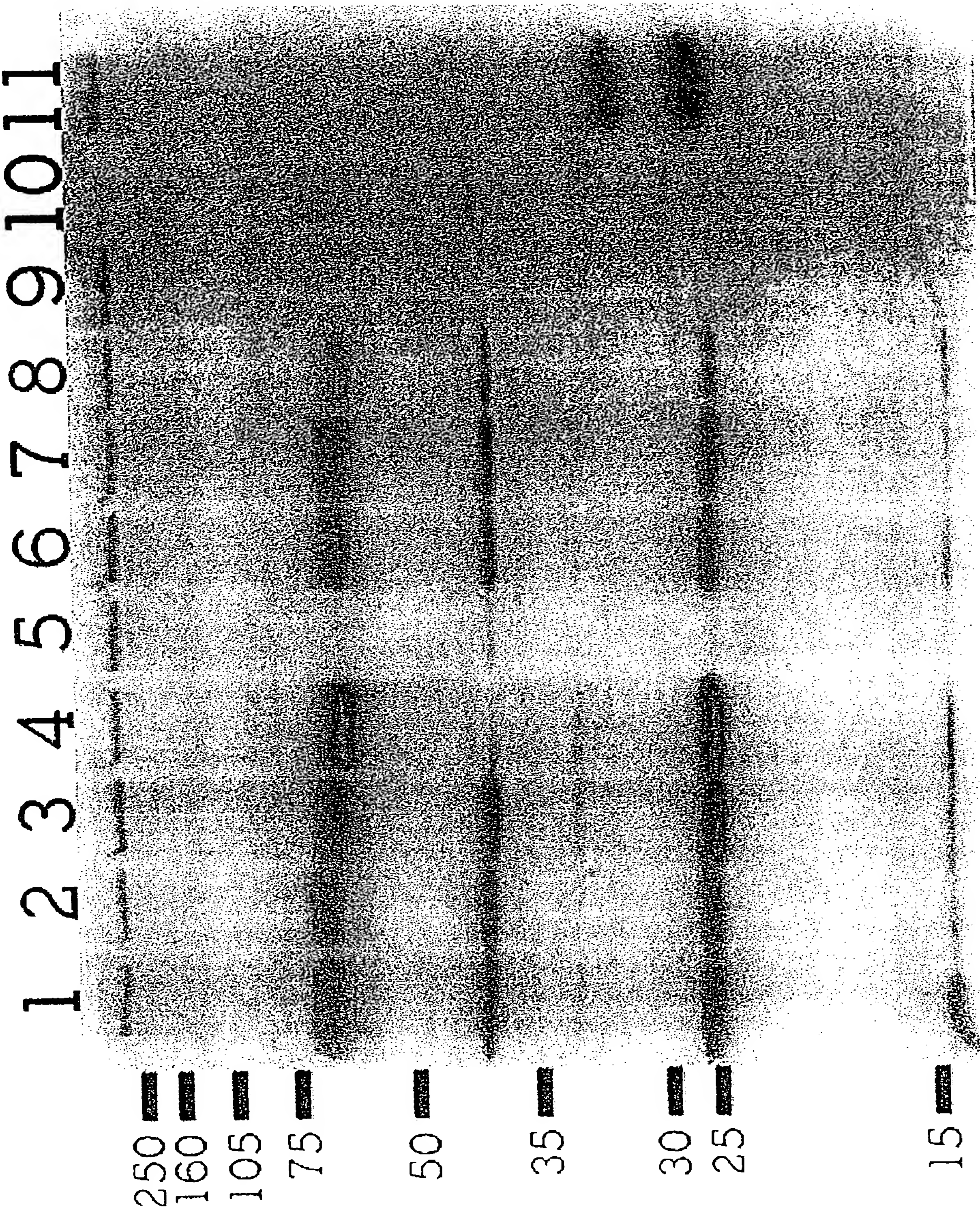
8% SDS-PAGE reducing gel

Fig 21 (3) Immuno-precipitation of metabolically labelled transient transfectants



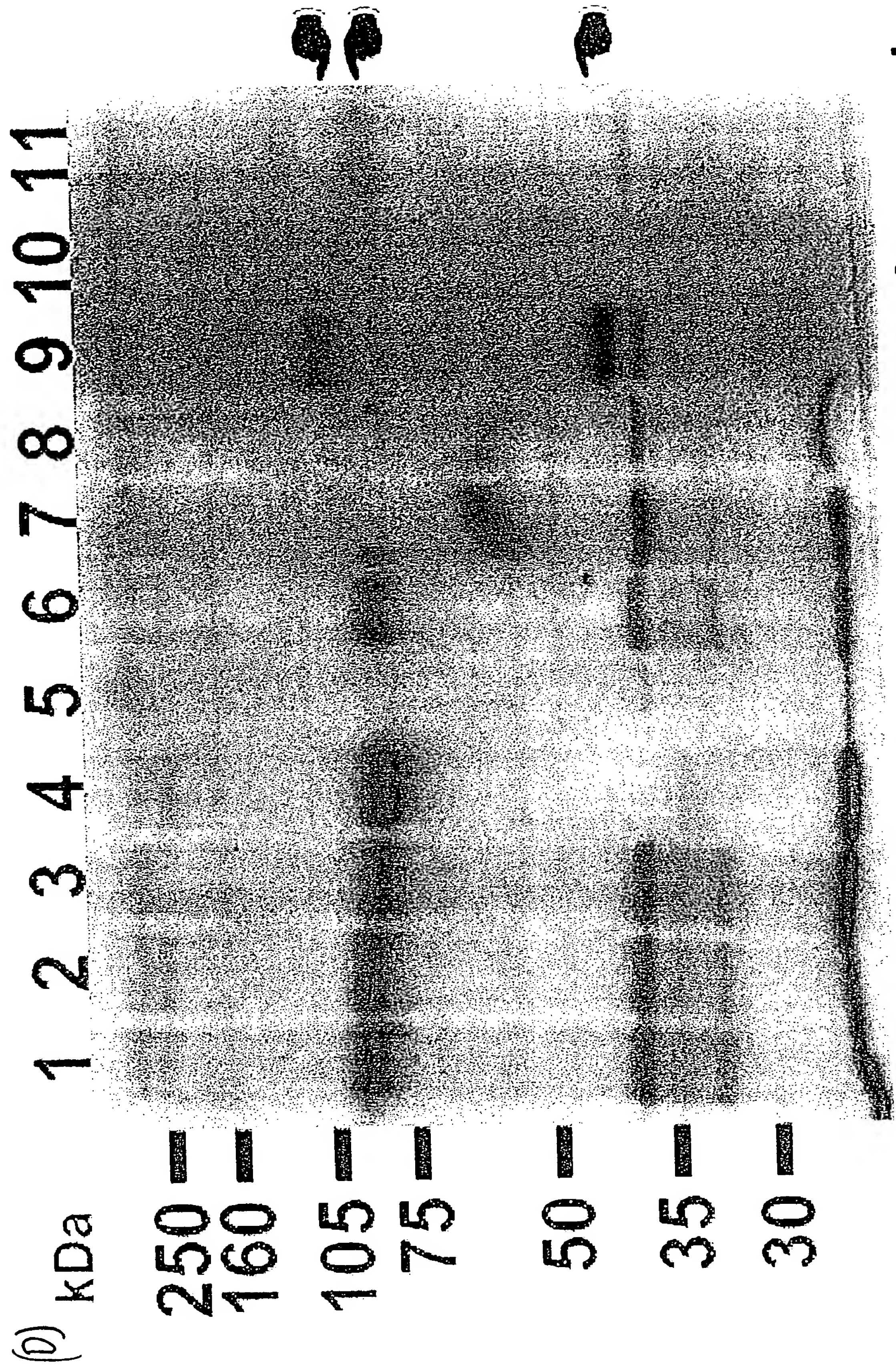
non-reducing gel

FIG 21 Immuno-precipitation of metabolically labelled transient transfectants



10% SDS-PAGE reducing gel

FIG-21 Immuno-precipitation of metabolically labelled transient transfectants



8% SDS-PAGE non-reducing gel

FIG 22

PDTRP binding assay standard curve (5' development)

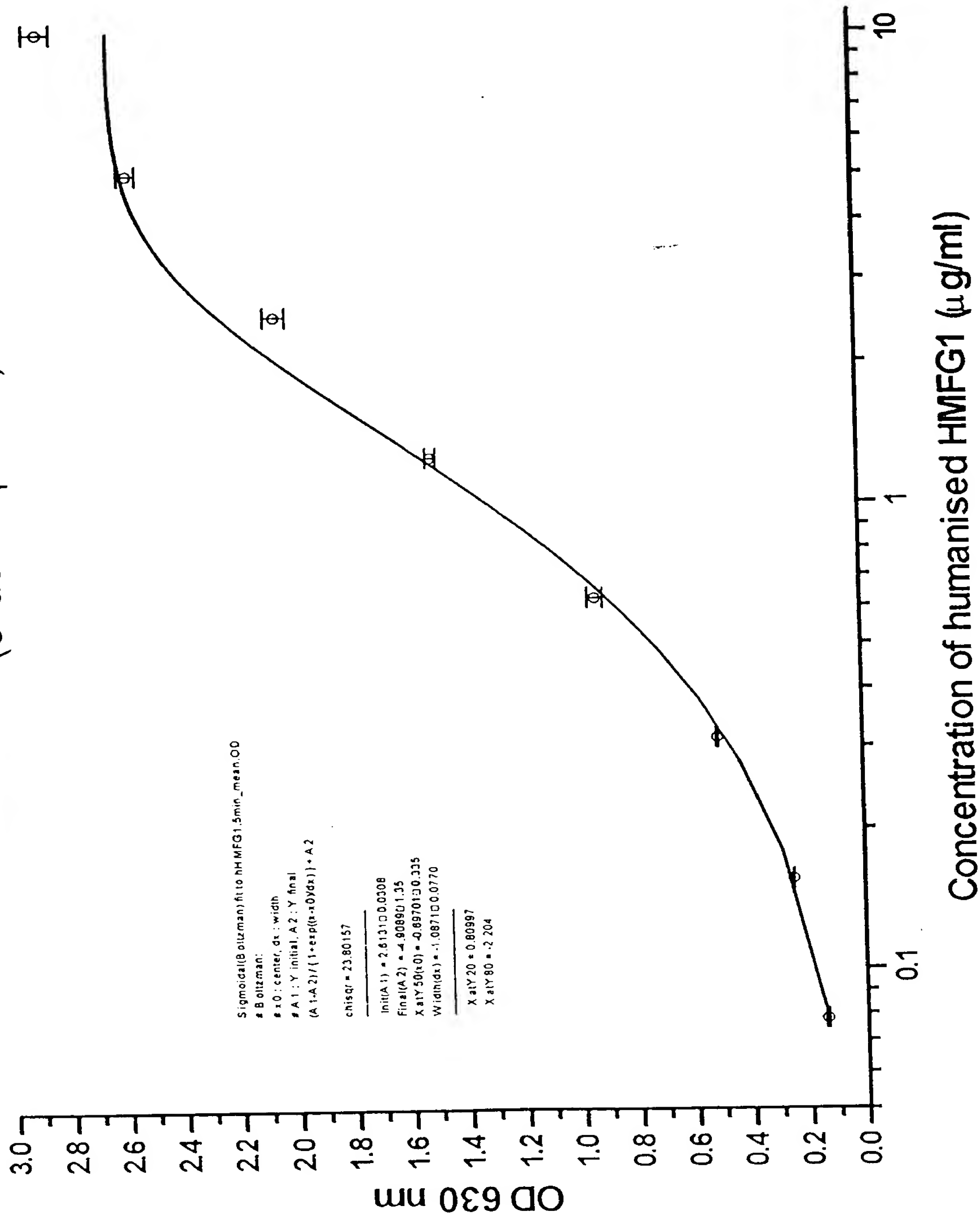


Fig 23

Corrected bovine DNase I standard curves at various time points

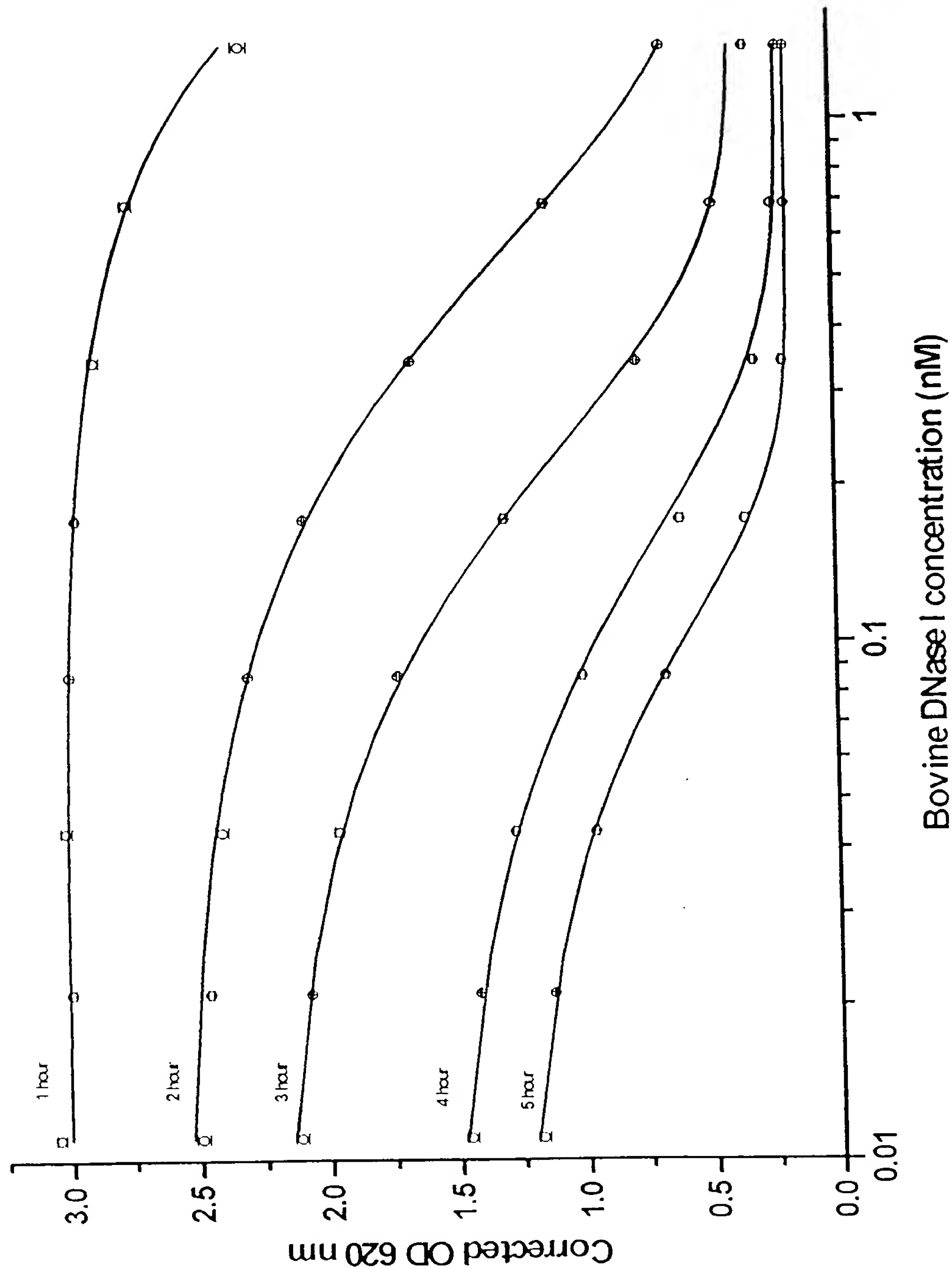


FIG 24

Corrected DNase I activity in transiently expressed
humanised human HMFG1-human DNase I constructs

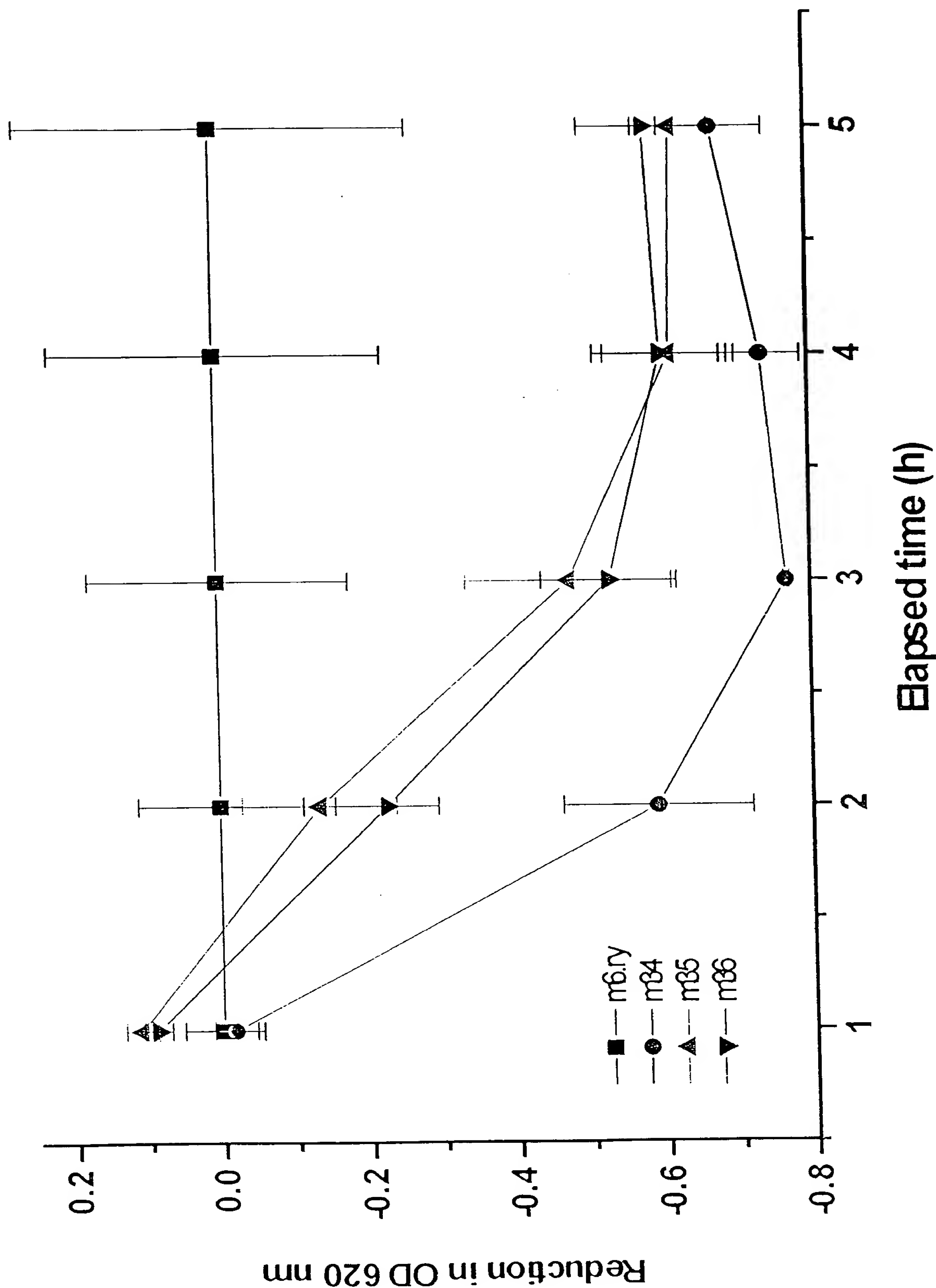


Fig 25

Corrected DNase I activity in transiently expressed
humanised HMFG1 F(ab')₂-human DNase I fusions

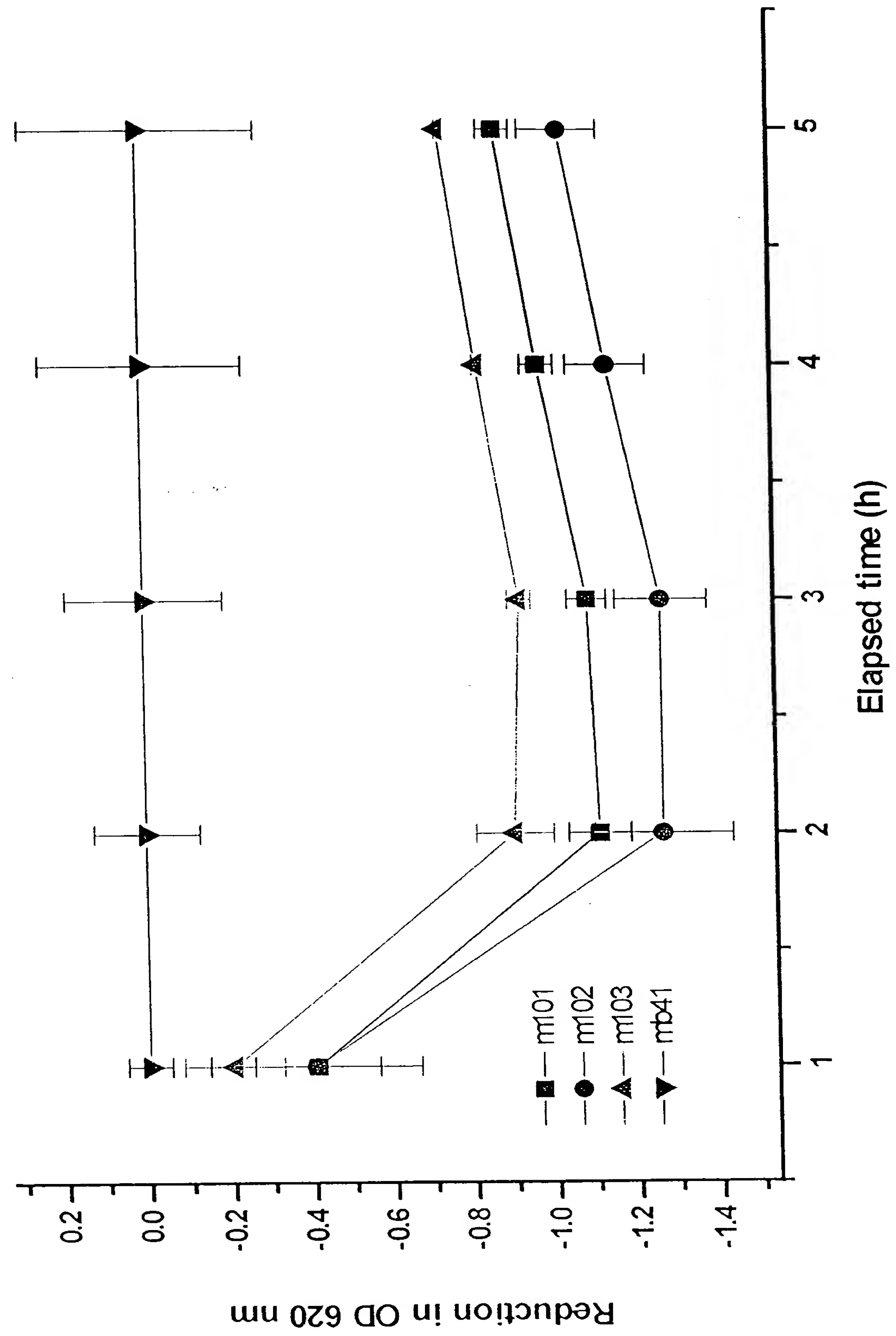
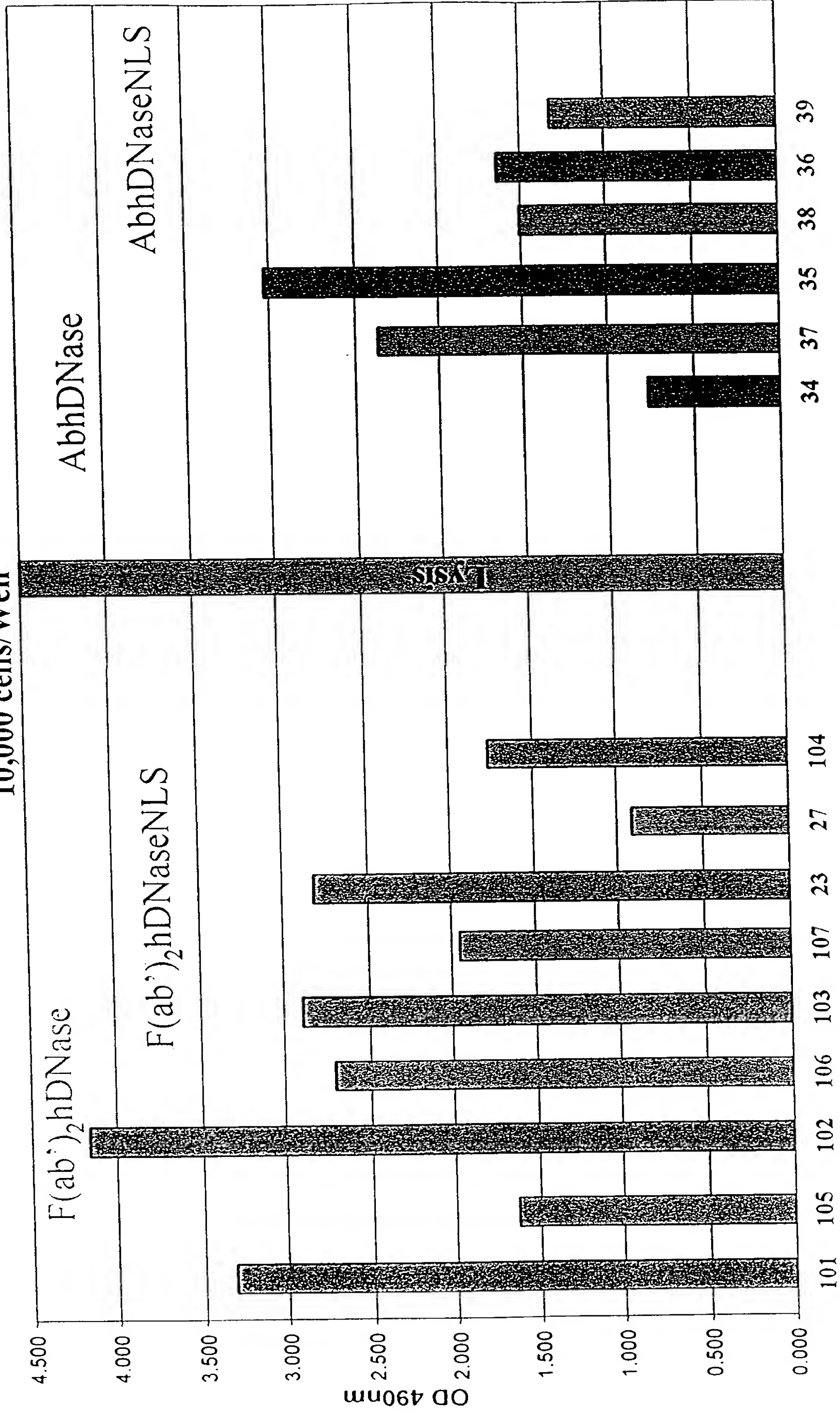


FIG. 26

Cytotoxicity Assay

10,000 cells/Well



0.097 µg/ml of each construct

Fig 27

MCF7 cells killed after 1h incubation with 1.35 ng of sample

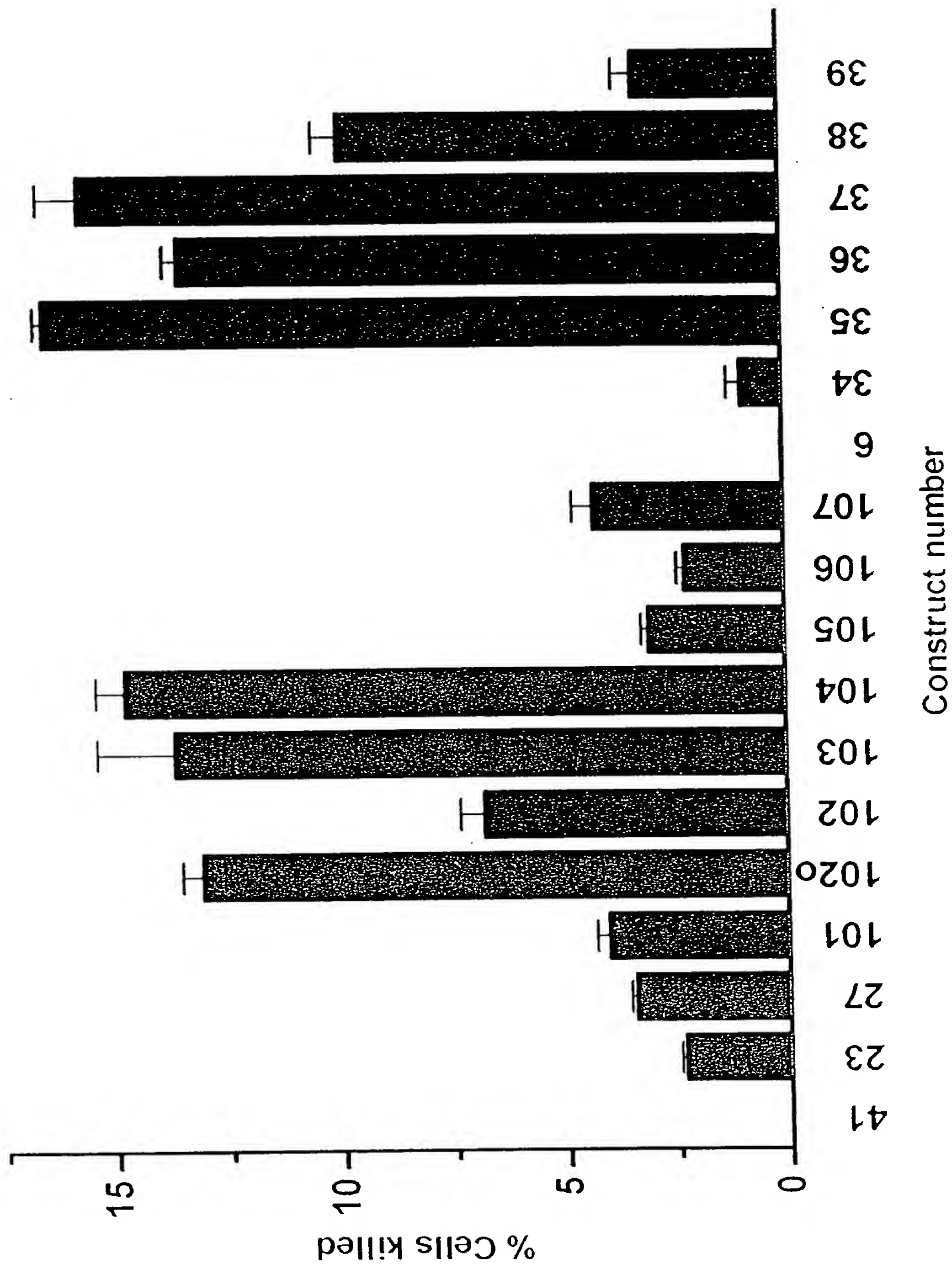


Figure 28

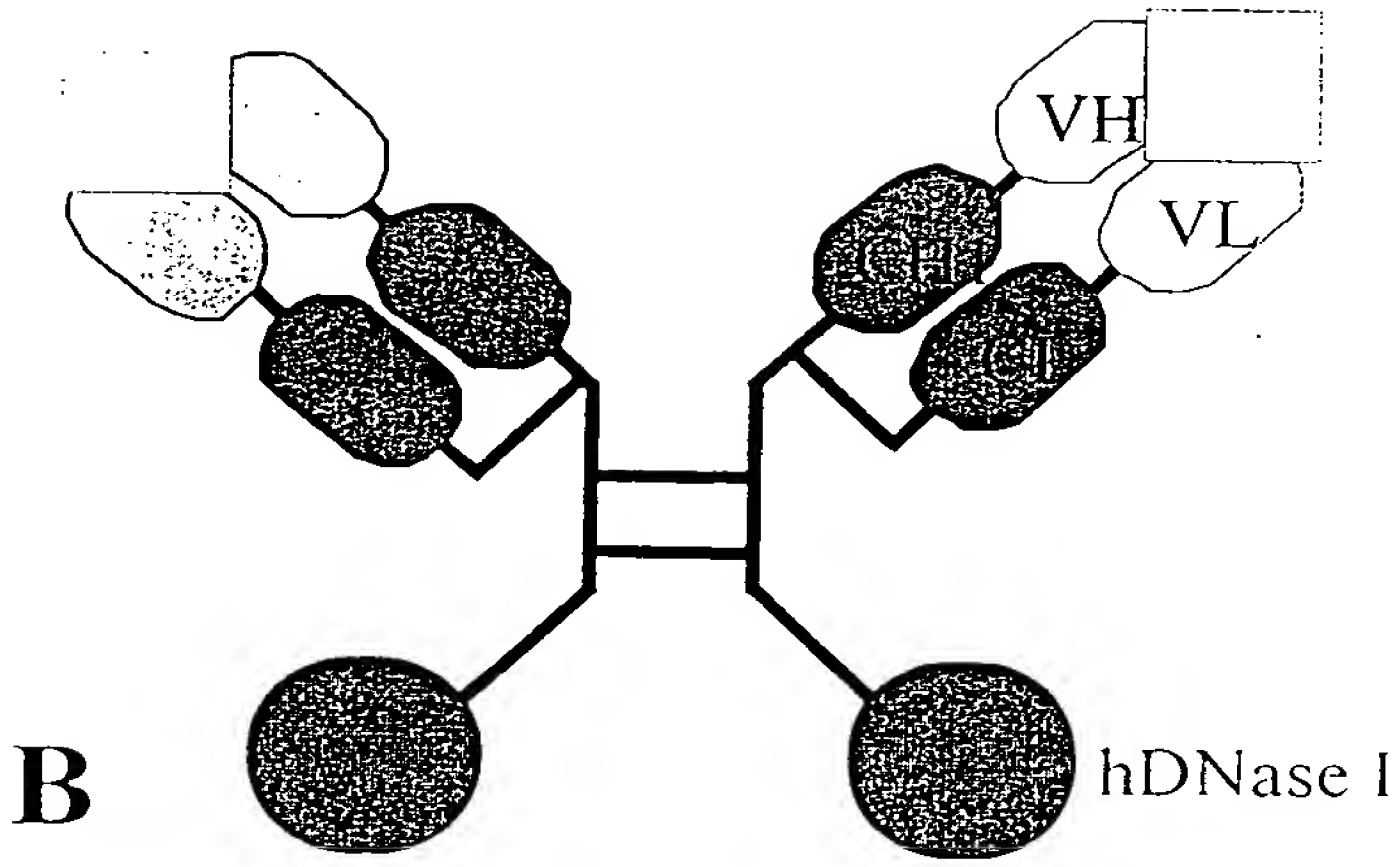
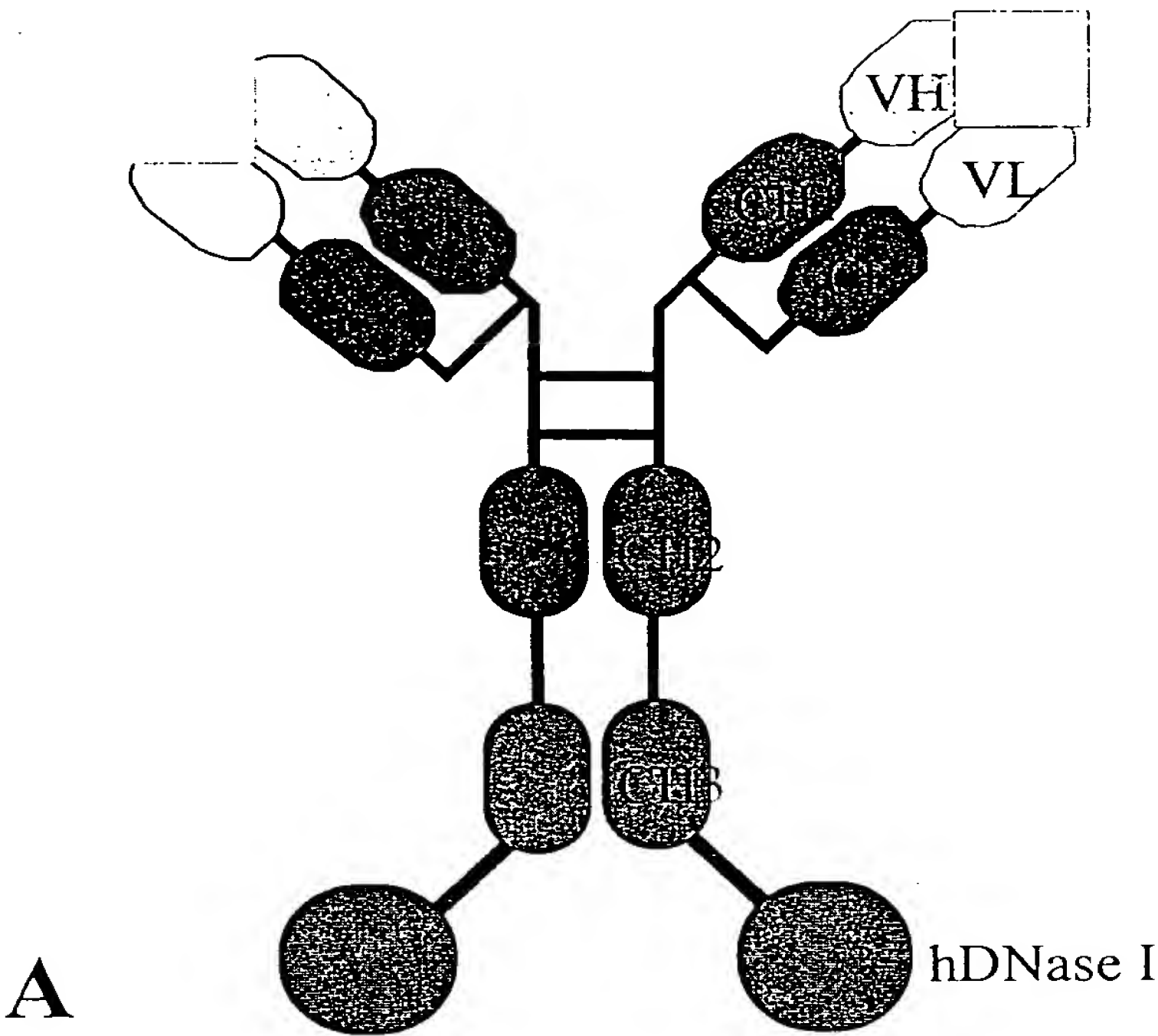
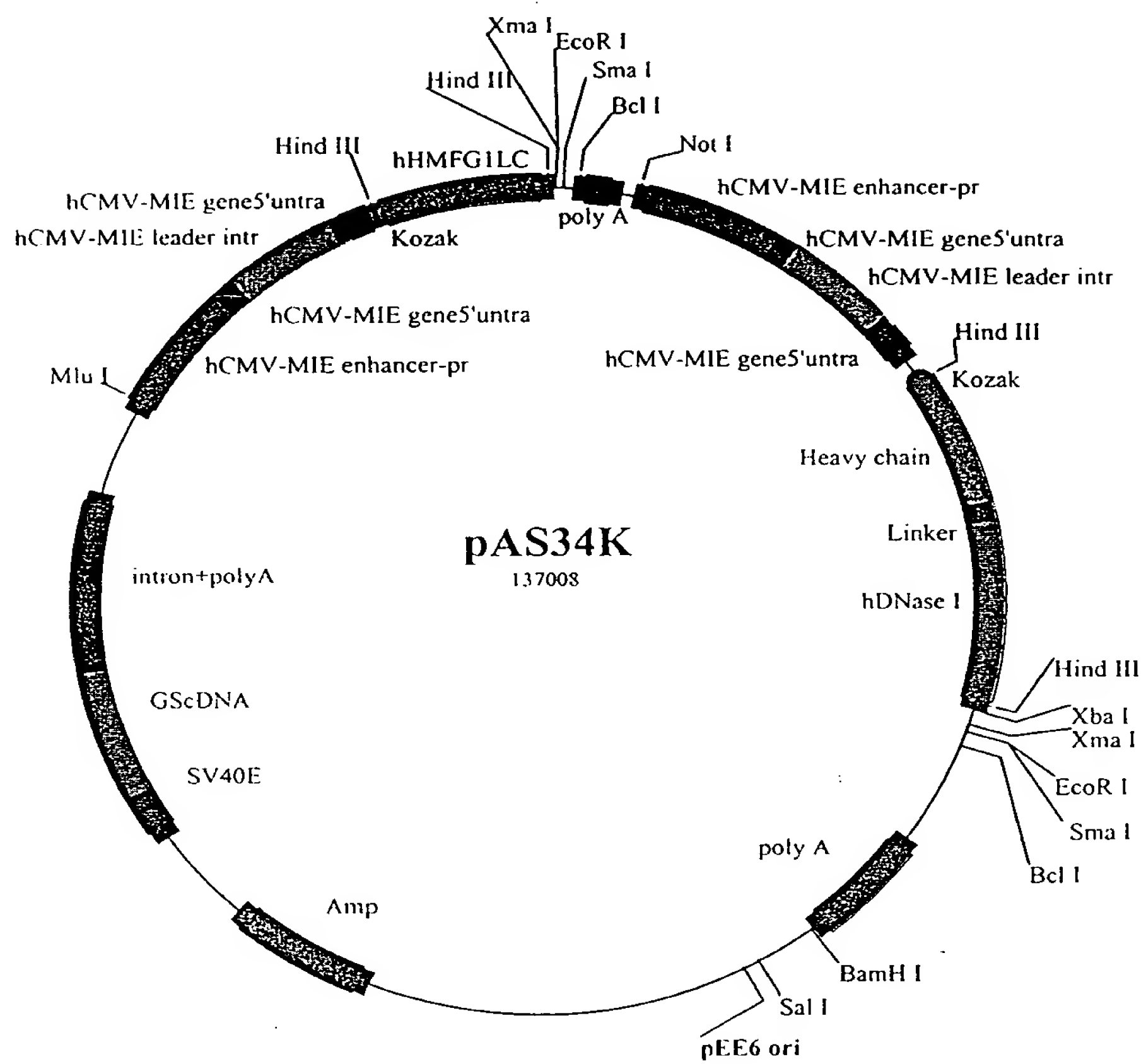
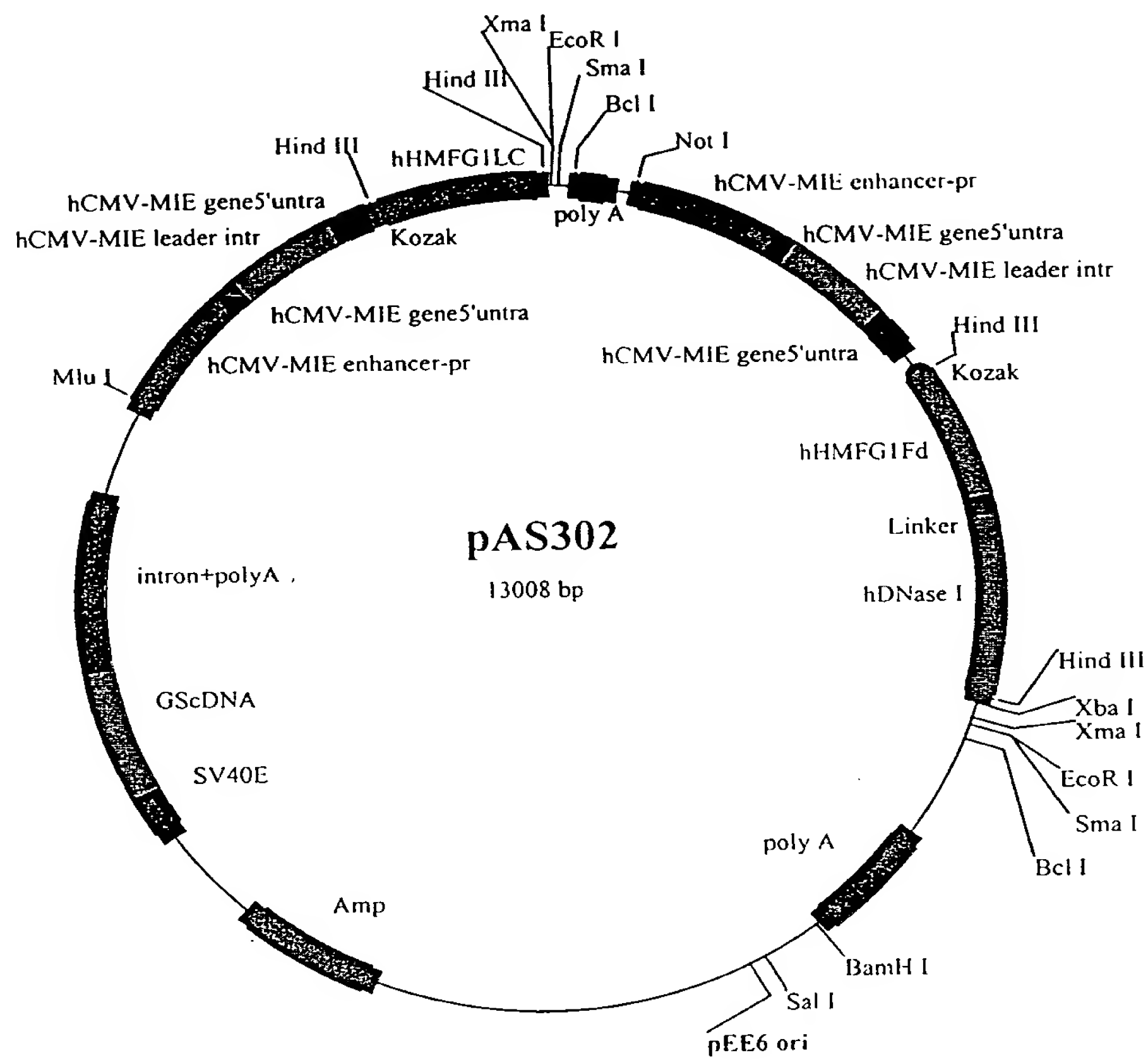


Figure 29



Ab-DNase

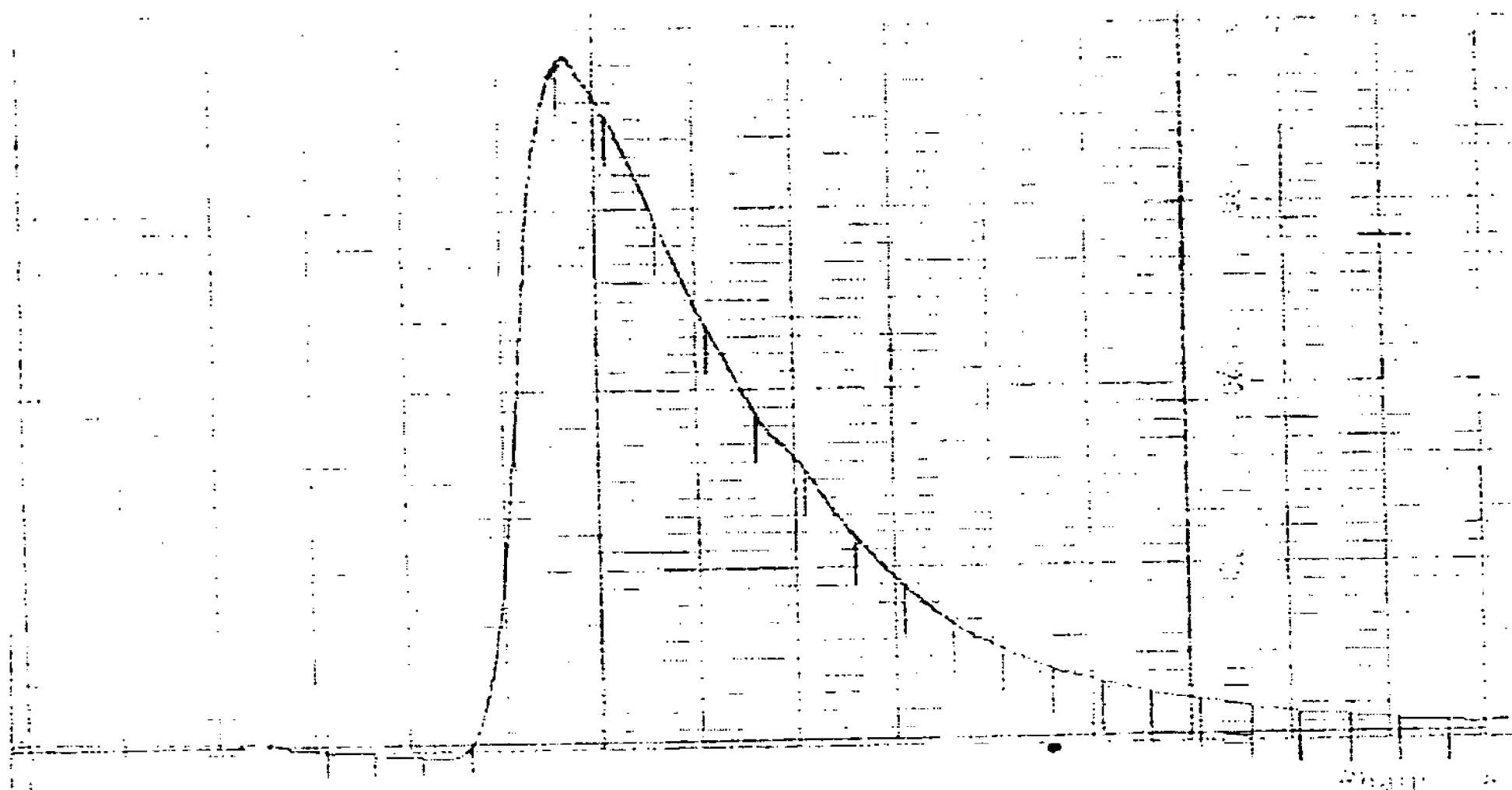
Figure 30



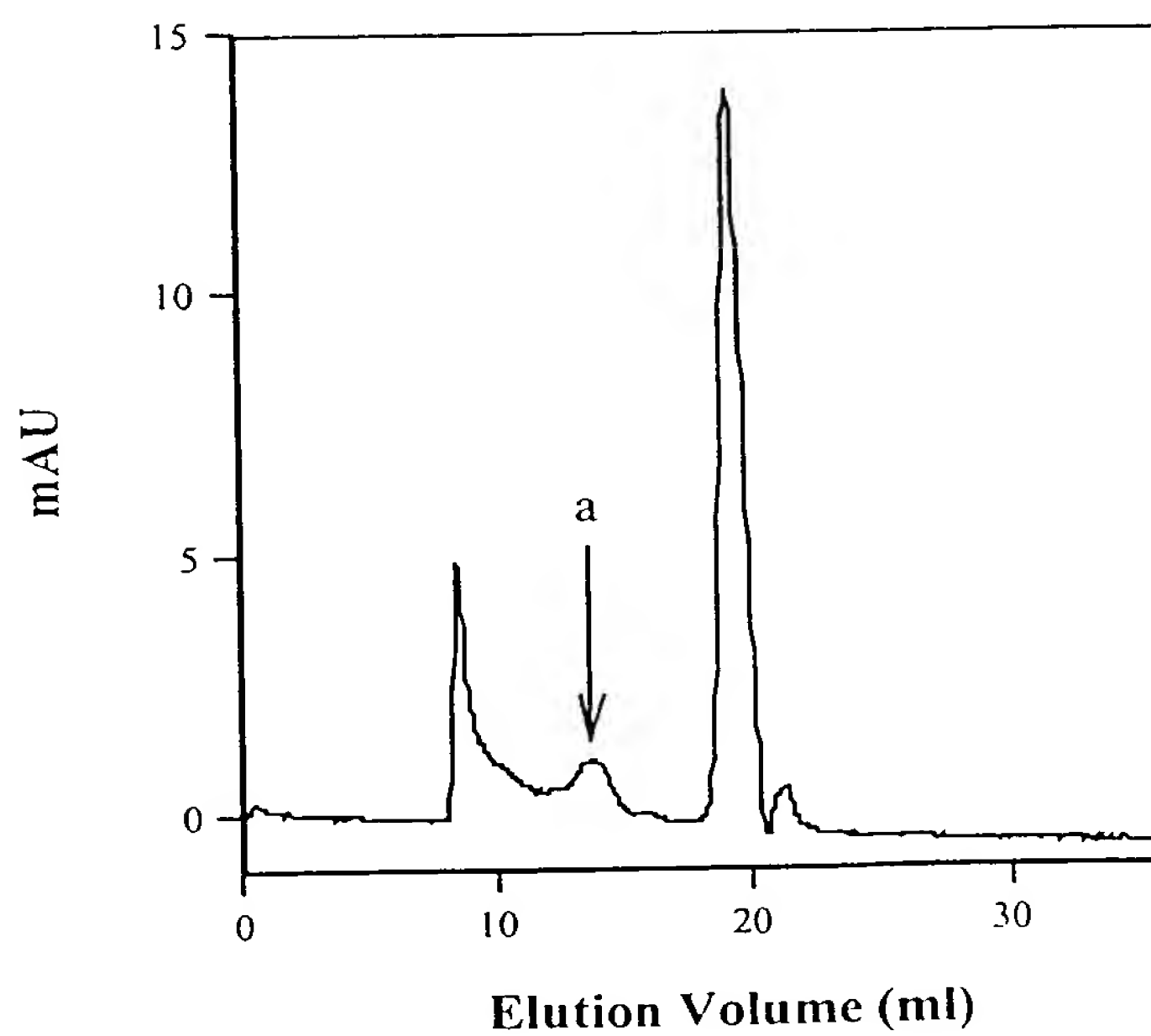
Fab-DNase

Figure 31

A

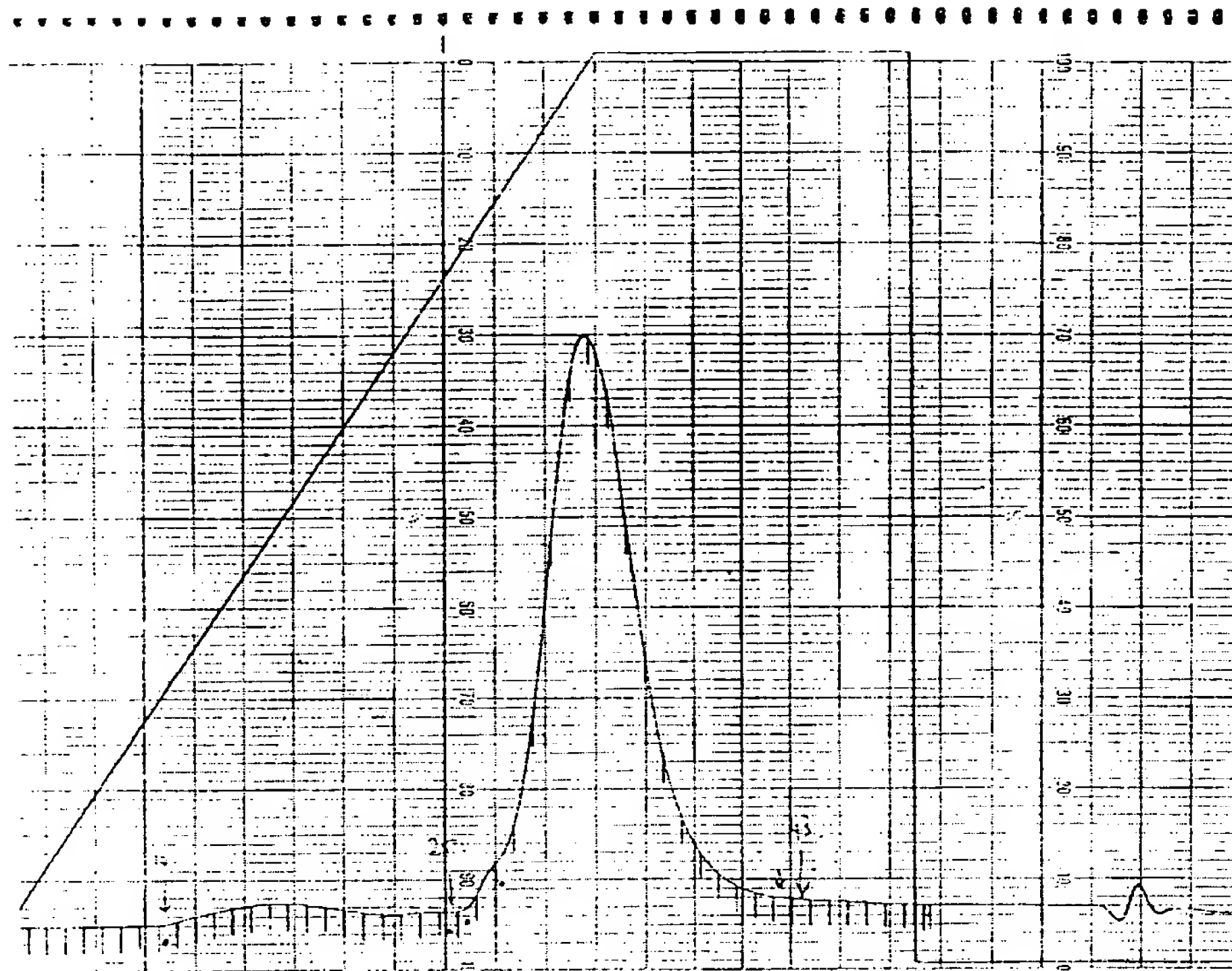


B



A

Figure 32



B

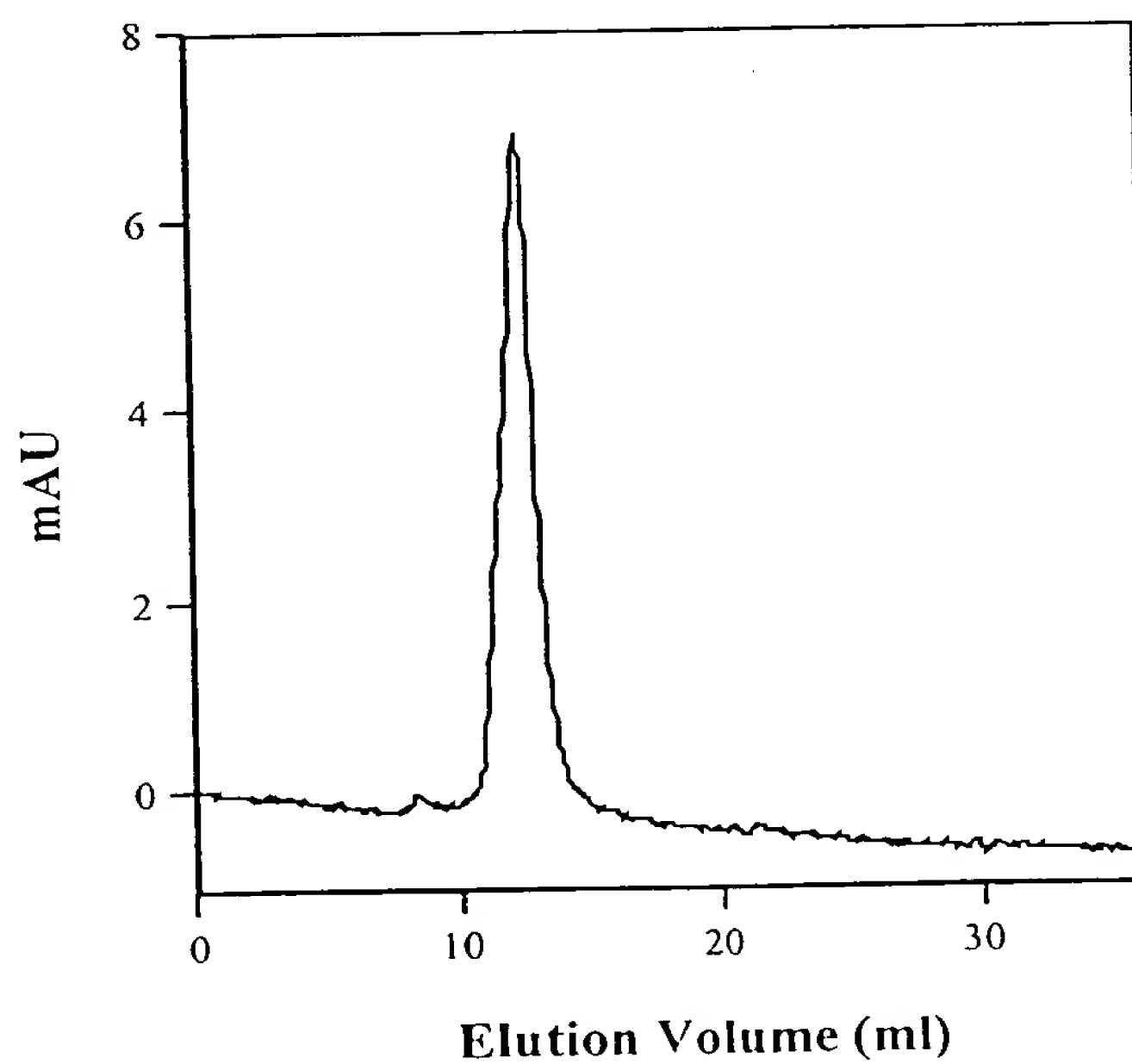


Figure 33

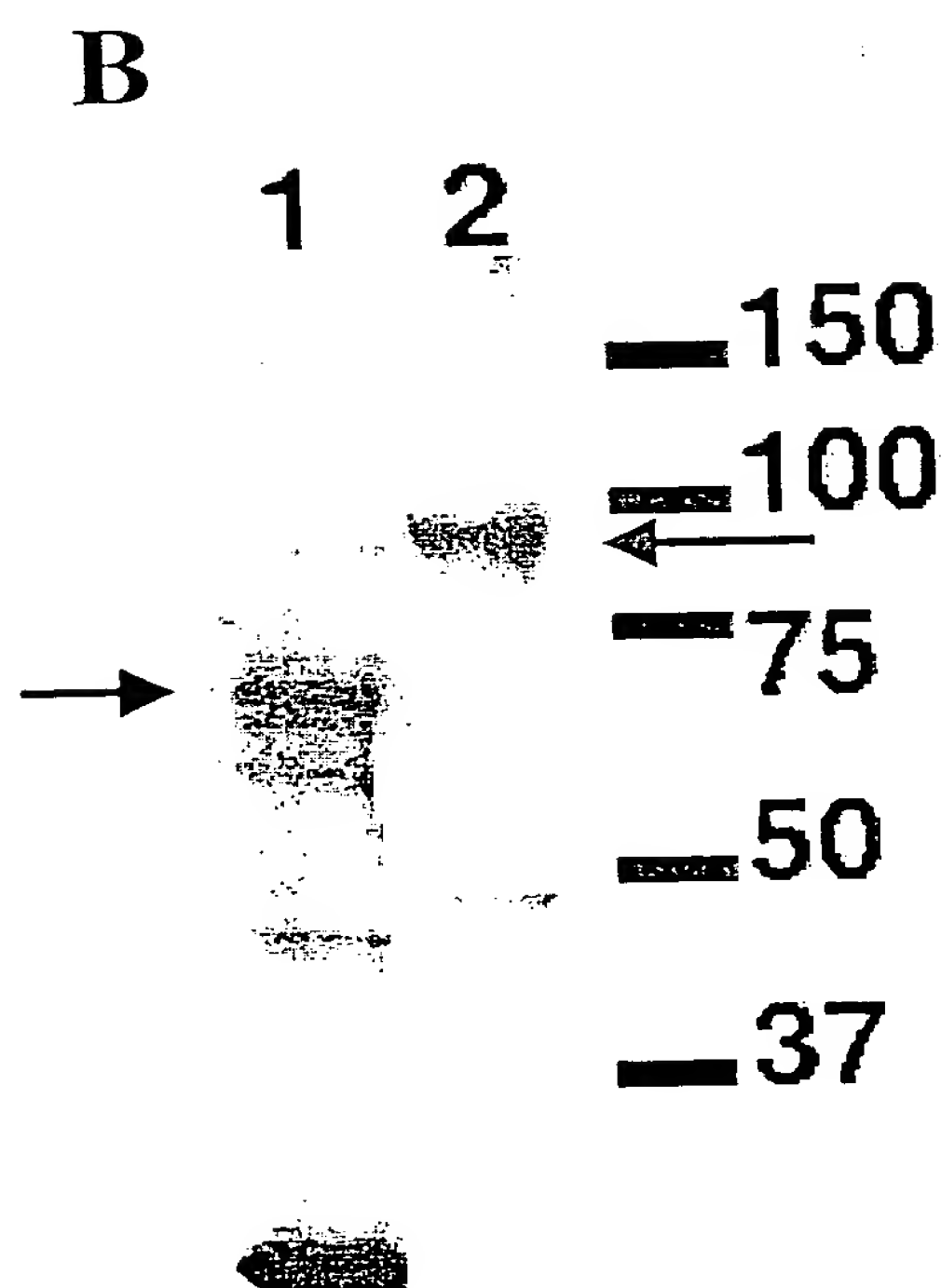
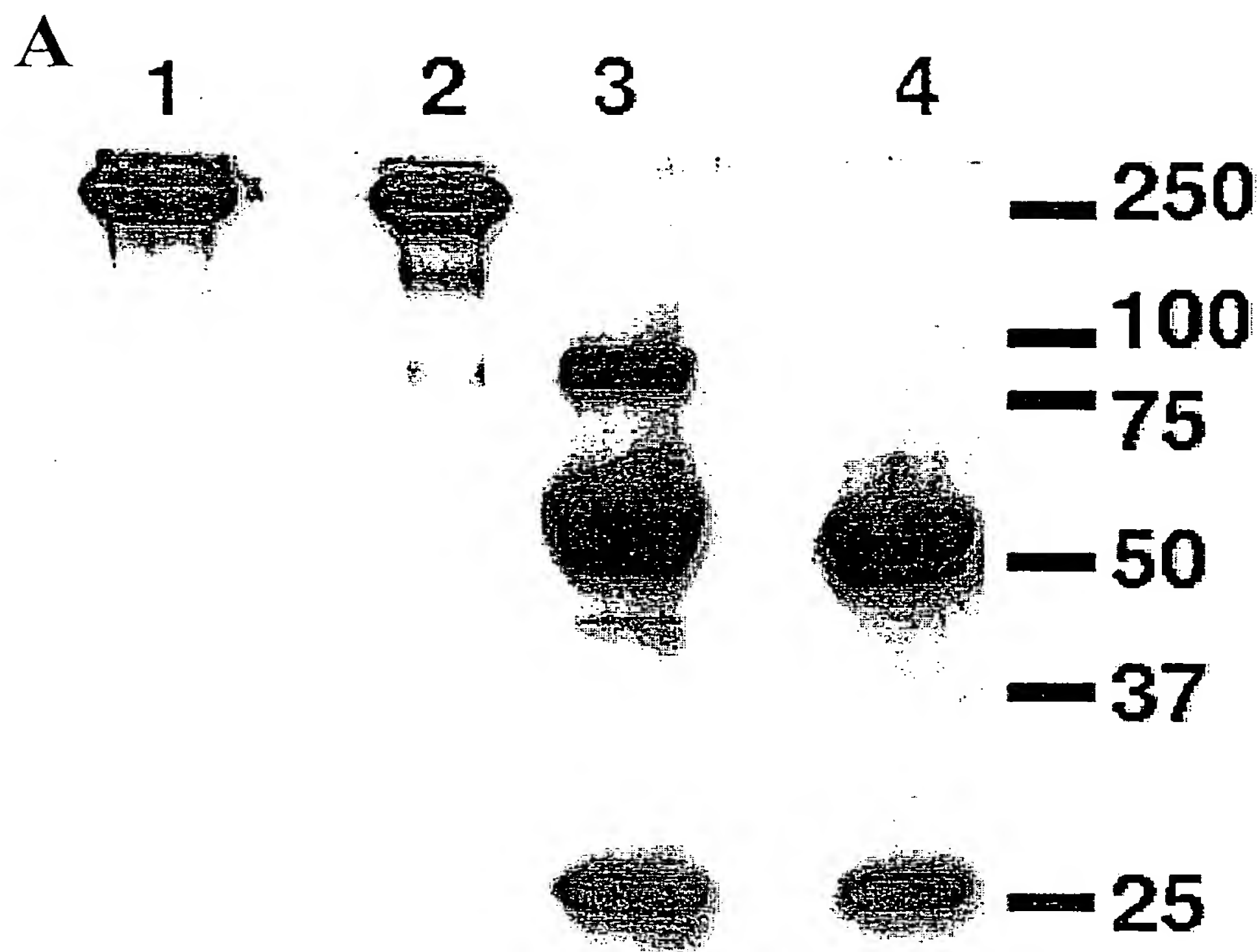
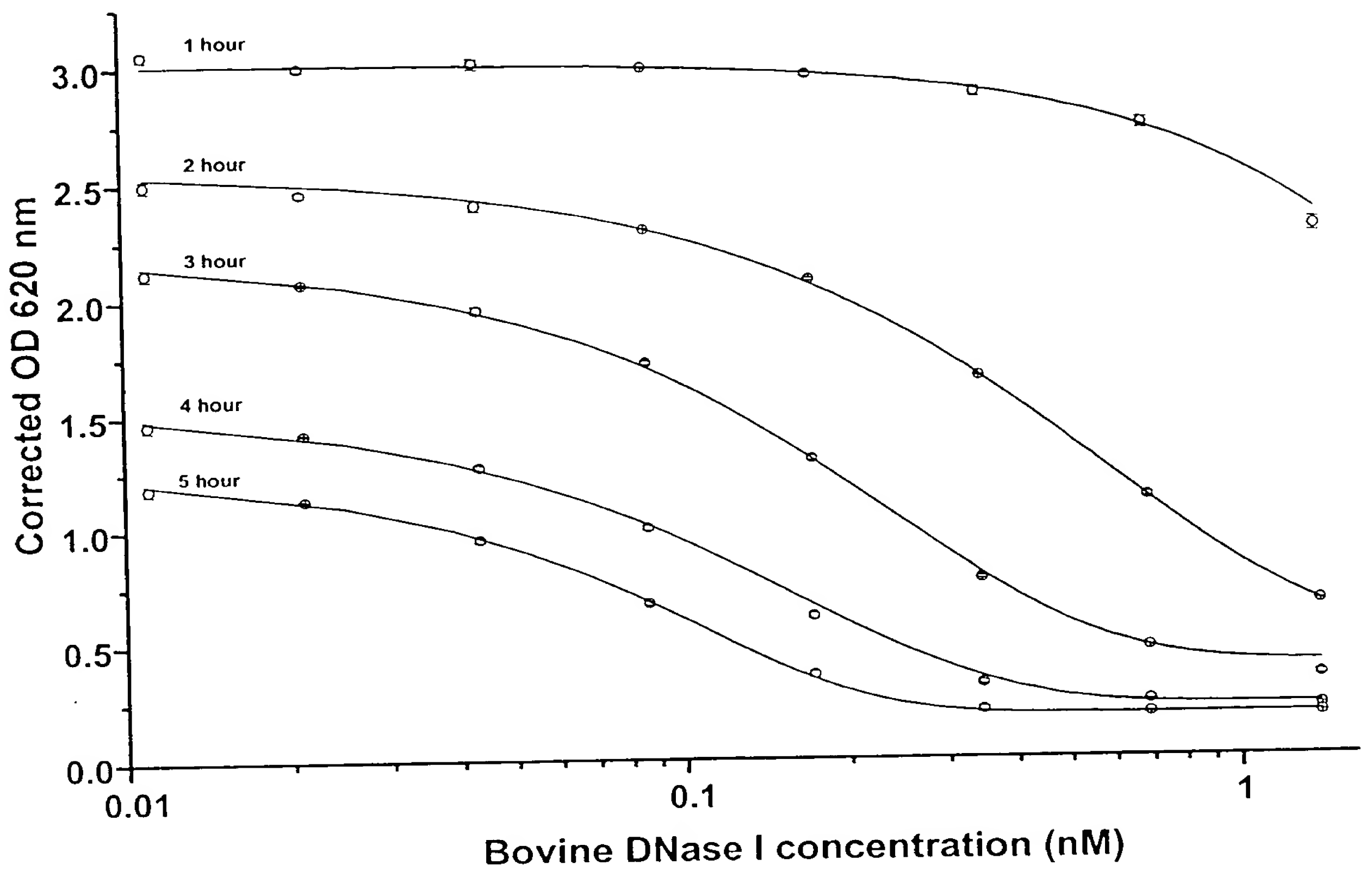


Figure 34

Bovine DNase I standard curves at various time points



A

Figure 34 – cont.

B

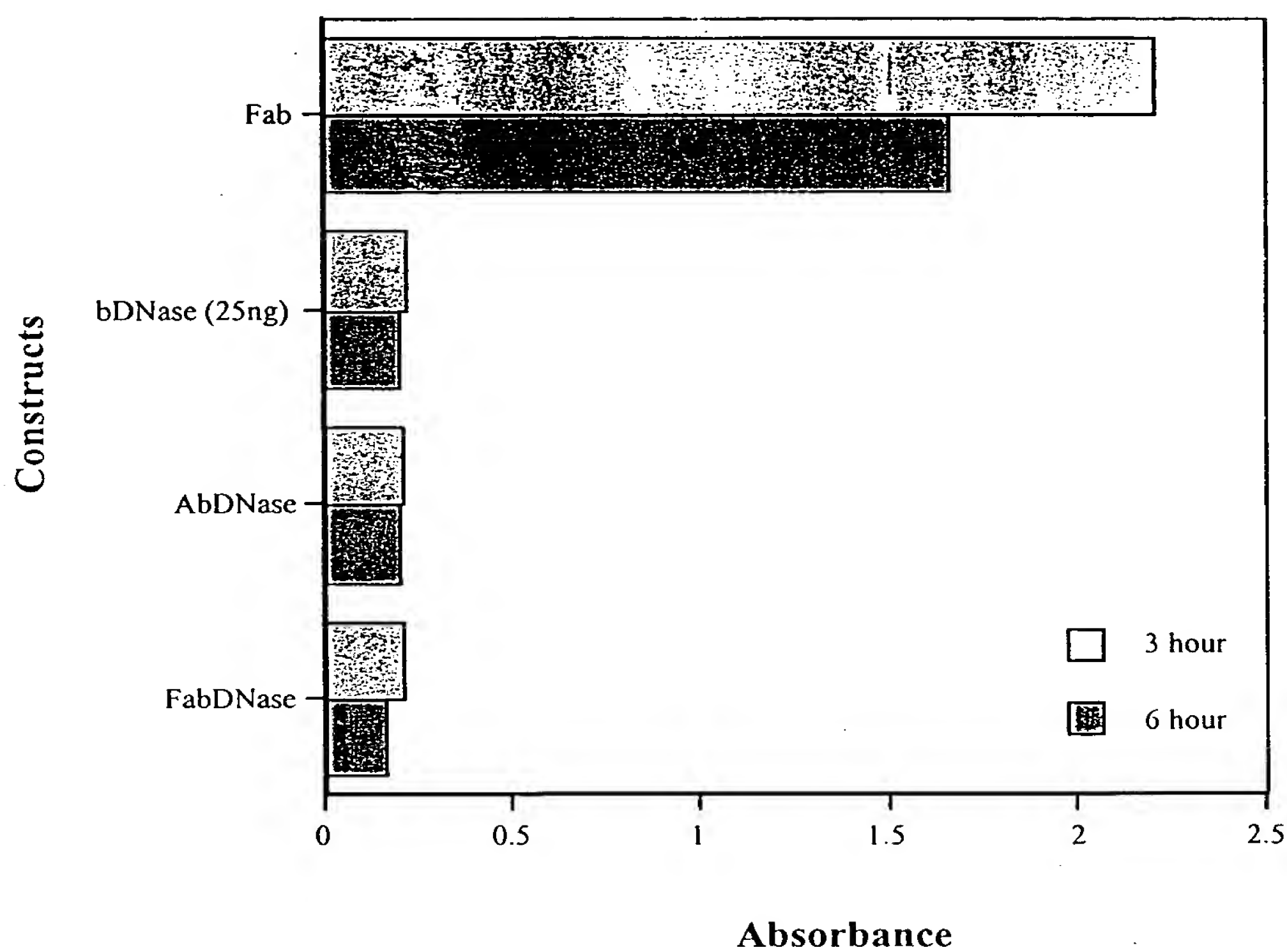


Figure 35

A

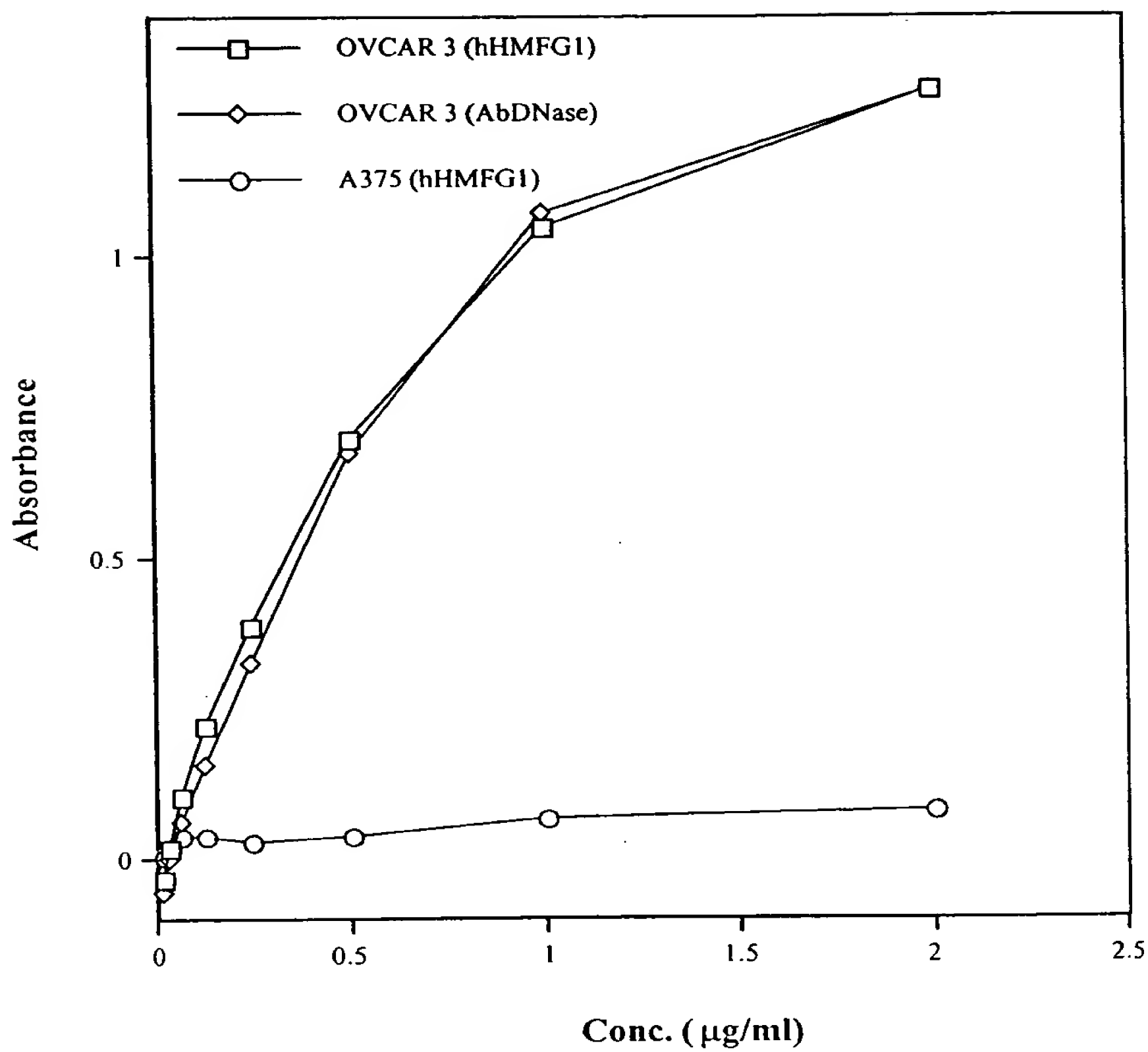
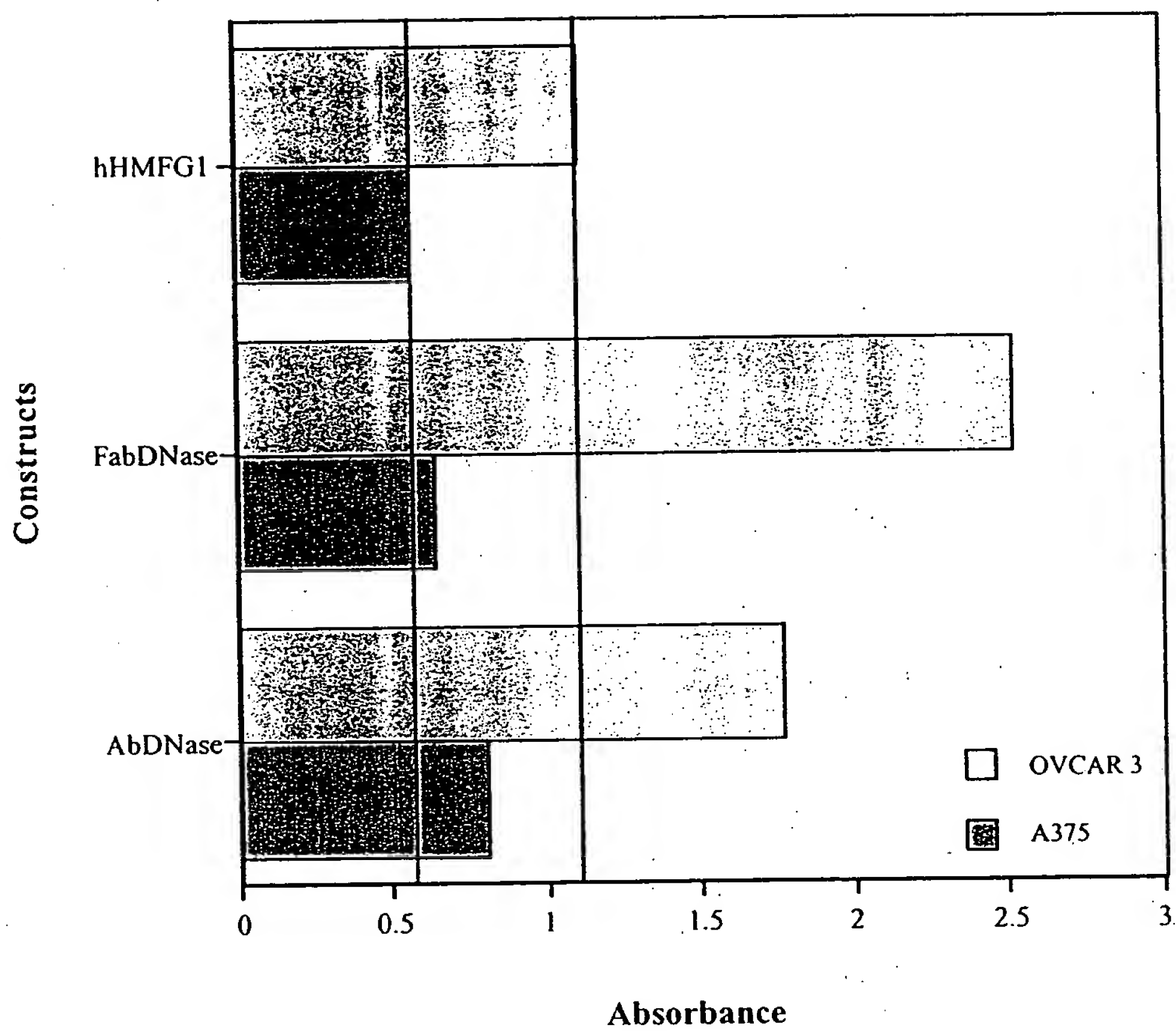


Figure 35 – cont.

B



BEST AVAILABLE COPY